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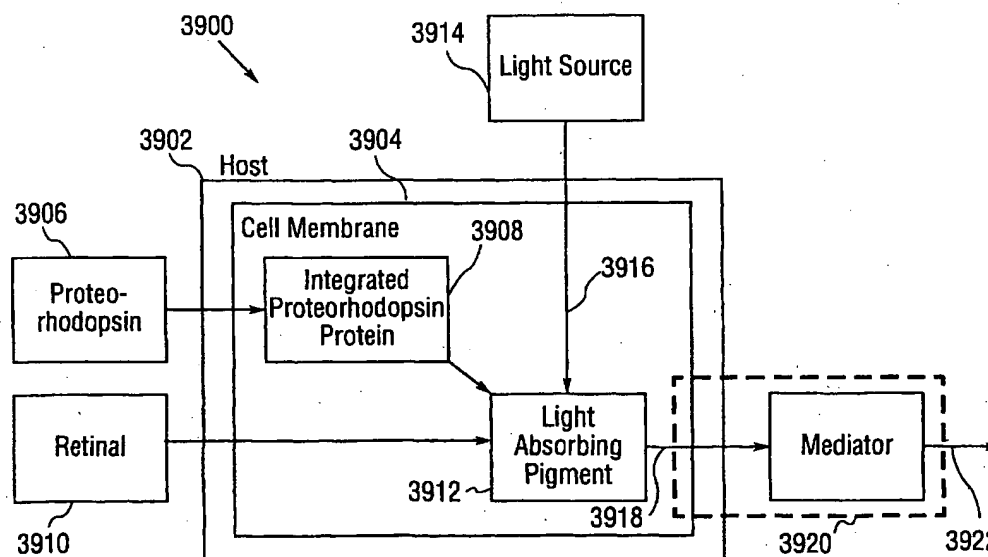
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(54) Title: LIGHT-DRIVEN ENERGY GENERATION USING PROTEORHODOPSIN



(57) Abstract: A light-driven energy generation system using proteorhodopsin is provided. Proteorhodopsin sequences were retrieved and amplified from naturally occurring members of the domain Bacteria using proteorhodopsin-specific polymerase chain reaction primers. Proteorhodopsin sequences were placed in expression vectors for production of proteorhodopsin proteins in a host, for instance, *E. coli* and other bacteria. The system also includes a light source and a source of retinal, that allows the system to convert light into biochemical energy. The generated biochemical energy could be mediated into electrical energy by a mediator.

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

PATENT APPLICATION

LIGHT-DRIVEN ENERGY GENERATION USING PROTEORHODOPSIN

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CROSS-REFERENCE TO RELATED APPLICATIONS

This application is cross-referenced to and claims priority from U.S. Provisional application 60/201,602 filed 05/03/2000, which is hereby incorporated by reference.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

This invention was supported in part by grant number OCE 0001619 from the National Science Foundation (NSF). The U.S. government has certain rights in the invention.

STATEMENT TO COMPUTER DISK AND SEQUENCE LISTING

This application includes a sequence listing of 65 sequences and a computer disk labeled "Sequence Listing for application entitled "Light-driven energy generation using proteorhodopsin" by Edward F. DeLong and Oded Beja" containing files "MBA101-SEQLIST.prj", dated "04/23/01" with 174,089 bytes, which is the PatentIn

project file generated using PatentIn Version 3.0 software provided by the USPTO, and "MBA101-SEQLIST.txt", dated "04/23/01" with 323,739 bytes, which is the generated sequence listing from the PatentIn project file MBA101-SEQLIST.prj using PatentIn Version 3.0 software, all which are herein incorporated. The information recorded in computer readable format on the incorporated computer disk labeled "Sequence Listing" containing files "MBA101-SEQLIST.prj" and "MBA101-SEQLIST.txt" are identical to the incorporated written sequence listing.

FIELD OF THE INVENTION

The present invention relates generally to gene expression of functional recombinant proteins in bacteria. More particularly, the present invention relates to proteorhodopsin genes and proteins that function as a light-driven energy generator in *Escherichia coli* (E. coli) and other bacteria.

BACKGROUND ART

Retinal (vitamin A aldehyde) is a chromophore that binds integral membrane proteins (opsins) to form light-absorbing pigments called rhodopsins. Rhodopsins are currently known to belong to two distinct protein families. The visual rhodopsins, found in the eye throughout the animal kingdom, are photosensory pigments. Archeal rhodopsins, found in extreme halophilic environments, function as light-driven protons pumps (bacteriorhodopsins), chloride ion pumps (halorhodopsins), or photosensory receptors (sensory rhodopsins). The two protein families show no significant sequence similarity and may have different origins. They do, however, share identical topologies characterized by seven transmembrane α -helices that form a pocket in which retinal is covalently linked, as a protonated Schiff base (helix G).

The archaeal rhodopsins are able to generate a photocycle which produces a chemiosmotic membrane potential in response to light, as such light energy is converted into biochemical energy. Recently, a protein with high sequence similarity to the archaeal rhodopsins has also been retrieved in the eukaryote *Neurospora crassa* (J.A. Bieszke et al., *Proceedings of National Academy of Sciences USA* 96:8034, 1999). The eucaryal rhodopsin formed a photochemically reactive pigment when bound to all-trans retinal and exhibited photocycle kinetics similar to those of archaeal sensory rhodopsins (J.A. Bieszke et al., *Biochemistry* 38:14138, 1999). To date, however, no rhodopsin-like sequences have been reported in members of the domain Bacteria, and no light-driven proton pumps based on rhodopsin have ever before been functionally expressed in *E. coli*.

The phototropic conversion of light energy into biochemical energy using bacteriorhodopsin can be harnessed for a variety of processes and applications, such as bio-electronic applications and bio-materials, as has been reported in US Patent No. 5,757,525 for optical devices, US Patent No. 5,854,710 for optical Fourier processing, and US Patent No. 5,470,690 for optical information storage. Bacteriorhodopsin in bio-electronic applications is aimed to interface, integrate, or substitute the silicon based microelectronics systems as well as molecular devices. Bacteriorhodopsin as a bio-material is integrated, for instance, in optical films for light mediated computer memory applications and pattern recognition.

Previously, archaeal rhodopsins capable of generating a chemiosmotic membrane potential in response to light had only been found in halophilic archaea. Therefore, rhodopsins that originate from archaea adapted to highly saline environments cannot be functionally expressed in *E. coli*. Finally, the isolation and cultivation of

halorhodopsins is an elaborate process. At present one does not foresee an economic utilization possible for this process (e.g. US Patent 5,290,699).

Accordingly, as one skilled in the art might readily acknowledge, there is a strong need to retrieve and provide rhodopsin-like sequences from naturally occurring members of the domain Bacteria.

OBJECTS AND ADVANTAGES

In light of the above, it is the primary objective of the present invention to provide rhodopsin-like sequences from naturally occurring members of the domain Bacteria. More specifically, it is the objective of the present invention to provide a method to retrieve proteorhodopsin genes from DNA of naturally occurring bacteria that encodes DNA sequence for proteorhodopsin proteins.

It is another objective of the present invention to provide proteorhodopsin-specific polymerase chain reaction primers that amplify the proteorhodopsin-containing gene from a DNA sample of naturally occurring bacteria.

It is yet another objective of the present invention to produce variants of a proteorhodopsin gene using the same proteorhodopsin-specific polymerase chain reaction primers by amplifying a proteorhodopsin-containing gene from of a mixed sample of naturally occurring bacteria.

It is still another objective of the present invention to provide an expression vector that produces a proteorhodopsin protein in *E. coli* and other bacteria.

It is another objective of the present invention to provide a light-driven energy generator in which the functional properties of proteorhodopsin are utilized. These properties include the ability to integrate within a host, for instance a cell membrane of *E. coli*, making an integrated proteorhodopsin protein, and the ability to bind retinal, making a light absorbing pigment.

It is another objective of the present invention to provide a light source and illuminate the light absorbing pigment to convert light energy into biochemical energy.

It is another objective of the present invention to provide a mediator and mediate the biochemical energy into electrical energy.

It is another objective of the present invention to provide methods to manipulate the kinetics of the light-driven energy generator.

The advantage of the present invention over the prior art is that it is not restricted to operate in halophilic archaea and could therefore be functionally expressed in *E. coli* and other bacteria. Accordingly, another advantage of the present invention is that it provides for a fast and cheap production method that allows for mass production of functionally active proteorhodopsin.

SUMMARY

The present invention provides proteorhodopsin gene and protein sequences retrieved from samples of naturally occurring members of the domain Bacteria. More specifically, the present invention provides a method for the retrieval and amplification of proteorhodopsin genes from DNA samples of naturally occurring marine bacteria. In accordance with several exemplary embodiments of the present invention, DNA samples were obtained from naturally occurring bacteria such as, for instance, marine proteobacteria, SAR86 bacteria, or recombinant DNA libraries containing naturally occurring bacteria. The present invention provides proteorhodopsin-specific polymerase chain reaction (PCR) primers to amplify a proteorhodopsin gene from DNA samples of these marine bacteria. The present invention also provides a device and method for the placement of proteorhodopsin genes in an expression vector to produce functional proteorhodopsin proteins in *E. coli* and other bacteria.

Accordingly, the present invention provides a method to produce and obtain variants of proteorhodopsin genes and proteins. The same proteorhodopsin-specific polymerase chain reaction primers amplify different variants of proteorhodopsin-containing genes from a mixed sample of naturally occurring bacteria. As one skilled in the art might readily acknowledge, these variants of a proteorhodopsin gene produce functional variations in the photocycle kinetics of the proteorhodopsin protein.

Furthermore, the present invention provides a light-driven energy generator that utilizes proteorhodopsin to convert light-energy into biochemical energy. This light-driven energy generator takes advantage of the functional properties of the proteorhodopsin protein once expressed in, for example, *E. coli* or other bacteria as is

described in exemplary embodiments. These properties include the ability to integrate within a host such as, for instance, a cell membrane of *E. coli* or other Bacteria, and thereby making an integrated proteorhodopsin protein or integrated cell membrane protein. These properties also include the ability to bind retinal and thereby making a light absorbing pigment. Illuminating the light absorbing pigment with a light source converts light energy into biochemical energy. Finally, the biochemical energy can be mediated into electrical energy by a mediator.

In accordance with exemplary embodiments, the present invention enables one skilled in the art to manipulate the kinetics of the proteorhodopsin protein photocycle once it is operational in the light-driven energy generator. In particular, the present invention provides examples in which the light source characteristics are manipulated. Examples are the manipulation of the delivery of fast-light pulses and/or the delivery of light at different wavelengths. The present invention also provides examples in which incremental additions of retinal influences the function of the light-driven energy generator. In addition, a proteorhodopsin gene or protein variant can be selected to determine an absorption spectra of the light absorbing pigment to change the kinetics of the light energy generator, for instance to meet a design/functional criteria of an application wherein proteorhodopsin is utilized.

BRIEF DESCRIPTION OF THE FIGURES

The objectives and advantages of the present invention will be understood by reading the following detailed description in conjunction with the drawings, in which:

- FIG. 1** illustrates the phylogenetic tree of bacterial 16S rRNA gene sequences including that encoded on the 130 kb bacterioplankton BAC clone (EBAC31A8).
- FIG. 2** provides a nucleotide sequence of polymerase chain reaction primer 1 (Sequence ID No:2) used to amplify a proteorhodopsin gene.
- FIG. 3** provides a nucleotide sequence of polymerase chain reaction primer 2 (Sequence ID No:3) used to amplify a proteorhodopsin gene.
- FIG. 4** provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:4) amplified from clone EBAC31A8 (Sequence ID No:1) using PCR primers 1 (Sequence ID No:2) and 2 (Sequence ID No:3), and the deduced amino acid sequence (Sequence ID No:5) of the proteorhodopsin gene Sequence ID No:4 amplified from clone EBAC31A8 (Sequence ID No:1).
- FIG. 5** provides a map of the secondary structure of the proteorhodopsin protein (Sequence ID No:7). Single letter amino acid codes are used (according to J. Sasaki and J.L. Spudich, Biophys. J. 75:2435, 1998). Predicted retinal binding pocket residues are marked in black.
- FIG. 6** provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:8) amplified from clone EBAC40E8 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:9) of the proteorhodopsin gene Sequence ID No:8 amplified from clone EBAC40E8.
- FIG. 7** provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:10) amplified from clone EBAC41B4 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:11) of the proteorhodopsin gene Sequence ID No:7 amplified from clone EBAC41B4.

FIG. 8 provides the nucleotide sequence of the proteorhodopsin gene (**Sequence ID No:12**) amplified from clone EBAC64A5 using PCR primers 1 (**Sequence ID No:2**) and 2 (**Sequence No:3**), and the deduced amino acid sequence (**Sequence ID No:13**) of the proteorhodopsin gene **Sequence ID No:12** amplified from clone EBAC64A5.

FIG. 9 provides a variants map of the DNA sequences of the proteorhodopsin gene with **Sequence ID No:4**, **Sequence ID No:8**, **Sequence ID No:10**, and **Sequence ID No:12** that were amplified from clone EBAC38A8, EBAC40E8, EBAC41B4 and EBAC64A5 respectively using the proteorhodopsin-specific PCR primer 1 (**Sequence ID No:2**) and 2 (**Sequence ID No:3**). Dots represent sequences having identical sequence as those in **Sequence ID No:4**.

FIG. 10 provides a variant map of the deduced amino acid sequences encoded by the proteorhodopsin gene with **Sequence ID No:4**, **Sequence ID No:8**, **Sequence ID No:10**, and **Sequence ID No:12** that were amplified from respectively EBAC38A8, EBAC40E8, EBAC41B4 and EBAC64A5 using the proteorhodopsin-specific primer 1 (**Sequence ID No:2**) and 2 (**Sequence ID No:3**). Lower case represents the PCR primer sequence region. Dots represent residues having identical sequence as those in **Sequence ID No:5**.

FIG. 11 provides the nucleotide sequence of the proteorhodopsin gene (**Sequence ID No:14**) amplified from clone HOT0m1 using PCR primers 1 (**Sequence ID No:2**) and 2 (**Sequence No:3**), and the deduced amino acid sequence (**Sequence ID No:15**) of the proteorhodopsin gene **Sequence ID No:14** amplified from clone HOT0m1.

FIG. 12 provides the nucleotide sequence of the proteorhodopsin gene (**Sequence ID No:16**) amplified from clone HOT75m1 using PCR primers 1 (**Sequence ID**

No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:17) of the proteorhodopsin gene Sequence ID No:16 amplified from clone HOT75m1.

FIG. 13 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:18) amplified from clone HOT75m3 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:19) of the proteorhodopsin gene Sequence ID No:18 amplified from clone HOT75m3.

FIG. 14 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:20) amplified from clone HOT75m4 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:21) of the proteorhodopsin gene Sequence ID No:20 amplified from clone HOT75m4.

FIG. 15 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:22) amplified from clone HOT75m8 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:23) of the proteorhodopsin gene Sequence ID No:22 amplified from clone HOT75m8.

FIG. 16 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:24) amplified from clone MB0m1 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:25) of the proteorhodopsin gene Sequence ID No:24 amplified from clone MB0m1.

FIG. 17 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:26) amplified from clone MB0m2 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence

(Sequence ID No:27) of the proteorhodopsin gene Sequence ID No:26 amplified from clone MB0m2.

FIG. 18 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:28) amplified from clone MB20m2 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:29) of the proteorhodopsin gene Sequence ID No:28 amplified from clone MB20m2.

FIG. 19 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:30) amplified from clone MB20m5 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:31) of the proteorhodopsin gene Sequence ID No:30 amplified from clone MB20m5.

FIG. 20 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:32) amplified from clone MB20m12 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:33) of the proteorhodopsin gene Sequence ID No:32 amplified from clone MB20m12.

FIG. 21 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:34) amplified from clone MB40m1 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:35) of the proteorhodopsin gene Sequence ID No:34 amplified from clone MB40m1.

FIG. 22 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:36) amplified from clone MB40m5 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence

(Sequence ID No:37) of the proteorhodopsin gene Sequence ID No:36 amplified from clone MB40m5.

FIG. 23 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:38) amplified from clone MB40m12 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:39) of the proteorhodopsin gene Sequence ID No:38 amplified from clone MB40m12.

FIG. 24 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:40) amplified from clone MB100m5 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:41) of the proteorhodopsin gene Sequence ID No:40 amplified from clone MB100m5.

FIG. 25 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:42) amplified from clone MB100m7 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:43) of the proteorhodopsin gene Sequence ID No:42 amplified from clone MB100m7.

FIG. 26 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:44) amplified from clone MB100m9 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:45) of the proteorhodopsin gene Sequence ID No:44 amplified from clone MB100m9.

FIG. 27 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:46) amplified from clone MB100m10 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence

(Sequence ID No:47) of the proteorhodopsin gene Sequence ID No:46 amplified from clone MB100m10.

FIG. 28 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:48) amplified from clone PALB1 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:49) of the proteorhodopsin gene Sequence ID No:48 amplified from clone PALB1.

FIG. 29 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:50) amplified from clone PALB2 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:51) of the proteorhodopsin gene Sequence ID No:50 amplified from clone PALB2.

FIG. 30 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:52) amplified from clone PALB5 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:53) of the proteorhodopsin gene Sequence ID No:52 amplified from clone PALB5.

FIG. 31 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:54) amplified from clone PALB7 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:55) of the proteorhodopsin gene Sequence ID No:54 amplified from clone PALB7.

FIG. 32 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:56) amplified from clone PALB6 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence

(Sequence ID No:57) of the proteorhodopsin gene Sequence ID No:56 amplified from clone PALB6.

FIG. 33 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:58) amplified from clone PALB8 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:59) of the proteorhodopsin gene Sequence ID No:58 amplified from clone PALB8.

FIG. 34 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:60) amplified from clone PALE1 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:61) of the proteorhodopsin gene Sequence ID No:60 amplified from clone PALE1.

FIG. 35 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:62) amplified from clone PALE6 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:63) of the proteorhodopsin gene Sequence ID No:62 amplified from clone PALE6.

FIG. 36 provides the nucleotide sequence of the proteorhodopsin gene (Sequence ID No:64) amplified from clone PALE7 using PCR primers 1 (Sequence ID No:2) and 2 (Sequence No:3), and the deduced amino acid sequence (Sequence ID No:65) of the proteorhodopsin gene Sequence ID No:64 amplified from PALE7.

FIG. 37 illustrates a phylogenetic tree of different proteorhodopsin genes.

FIG. 38 provides an example of an alignment of proteorhodopsin amino acid sequences.

FIG. 39 provides a light-driven energy generator that utilizes proteorhodopsin.

- FIG. 40** provides an example of a proteorhodopsin-expressing *E. coli* cell suspension (+) compared to control cells (-), both with all-*trans* retinal.
- FIG. 41** provides an example of absorption spectra of retinal-constituted proteorhodopsin in *E. coli* membranes and a negative control.
- FIG. 42** provides an example of a light-driven transport of protons by a proteorhodopsin-expressing *E. coli* cell suspension.
- FIG. 43** provides an example of a transport of [³H]TPP⁺ in *E. coli* right-side-out vesicles containing expressed proteorhodopsin, reconstituted with or without 10 μM retinal in the presence of light or in the dark.
- FIG. 44** provides an example of laser flash-induced absorbance changes in suspensions of *E. coli* membranes containing proteorhodopsin.
- FIG. 45** provides an example of absorption spectra of retinal-constituted proteorhodopsin in *E. coli* membranes.

DETAILED DESCRIPTION

Although the following detailed description contains many specifics for the purposes of illustration, anyone of ordinary skill in the art will appreciate that many variations and alterations to the following details are within the scope of the invention. Accordingly, the following preferred embodiment of the invention is set forth without any loss of generality to, and without imposing limitations upon, the claimed invention.

Proteorhodopsin

The present invention provides rhodopsin-like gene and protein sequences retrieved from naturally occurring members of the domain Bacteria. More specifically, the

present invention provides a method for the retrieval and amplification of proteorhodopsin genes from DNA samples of naturally occurring marine bacteria. In accordance with exemplary embodiments of the present invention, DNA samples were obtained from naturally occurring marine bacteria such as bacteria from the SAR86 group. Provided as an exemplary embodiment of the SAR86 group, DNA samples were obtained from a bacterioplankton Bacterial Artificial Chromosome (BAC) clone BAC31A8 (also referred to as EBAC31A08). In general, as will be appreciated by those of ordinary skill in the art, suitable DNA samples can also be obtained from other sources, e.g., from a marine environment or from a recombinant DNA library containing genomic fragments of samples of naturally occurring bacteria.

FIG. 1 shows the phylogenetic tree of bacterial 16S rRNA gene sequences including that encoded on the EBAC31A8. **FIG. 1** also shows the relationship of EBAC31A8 to the SAR86 bacteria group as well as to the gamma-proteobacteria group. A subclone shotgun library was constructed from BAC clone 31A8, and subclones were sequenced in both directions on the MegaBACE 1000 capillary array electrophoresis DNA sequencing instrument (Molecular Dynamics, Sunnyvale, CA). Sequence analysis of a 130-kb genomic DNA that encodes the ribosomal RNA operon from BAC31A8, reveals an open reading frame encoding a proteorhodopsin. In an exemplary embodiment, the contiguous sequence was assembled using SEQUENCHER 3.1.1 software (Gene Codes Co., Ann Arbor, MI). Other sequencing techniques can also be used, as will be recognized by those skilled in the art. The sequence of the proteorhodopsin-containing contig has been deposited in GenBank under accession #AF279106 and deposit date October 23rd, 2000. **Appendix A**, hereby incorporated, shows the nucleotide sequence of the BAC clone BAC31A8 (**Sequence ID No:1**)

which contains the 130 kilobases genomic DNA from a naturally occurring marine bacterium.

Proteorhodopsin was amplified from the 130 kilobase bacterioplankton BAC clone 31A8 (**Sequence ID No:1**) by polymerase chain reaction (PCR), using the proteorhodopsin-specific primers 5'-aCCATGGgtaaattattactgatattagg-3' (**Sequence ID No:2** and shown in **FIG. 2**) and 5'-agcattagaagattctttaacagc-3' (**Sequence ID No:3** and shown in **FIG. 3**). References for PCR are, for instance, *The Polymerase Chain Reaction*, Mullis et al., Ed. (Birkhauser, Boston, 1994) and U.S. Patent Nos. 4,683,195 and 4,683,202 to Mullis et al. The proteorhodopsin-specific PCR primers include the addition of 3 nucleotides that encoded one amino acid not found in the native gene sequence of clone BAC31A8 (**Sequence ID No:6**), in the second amino acid position which is a glycine located on the 2nd codon ("GGT"). Therefore, compare the second amino acid position in the **Sequence ID No:5** using PCR primers 1 and 2 with the native **Sequence ID no:7**. This addition of one non-native amino acid created a new restriction endonuclease site (NcoI site) not present in the native sequence. This allowed subcloning of the amplified fragment into the NcoI restriction site of an expression vector pBAD TOPO TA Cloning® Kit (Invitrogen, La Jolla, CA). The present invention is not limited to the use of this type of expression vector and other expression vectors could also be used.

FIG. 4 shows the nucleotide sequence of the proteorhodopsin gene (**Sequence ID No:4**) that results from amplification of the proteorhodopsin-containing DNA in BAC31A8 using proteorhodopsin-specific PCR primers **Sequence ID No:2** and **Sequence No:3**. **FIG. 4** also shows the deduced amino acid sequences (**Sequence ID No:5**) encoded by the proteorhodopsin gene (**Sequence ID No:4**).

FIG. 5 shows an exemplary embodiment of a secondary structure of proteorhodopsin after it has been folded in a cell membrane **510** and bonded with retinal **520**. **FIG. 5** shows the native proteorhodopsin gene (**Sequence ID No:6**) obtained from clone BAC31A8 and encodes a proteorhodopsin protein of 249 amino acids with a molecular weight of 27 kD (**Sequence ID No:7**). In **FIG. 5**, **530** indicates seven transmembrane domains, a typical feature of the rhodopsin protein family, that aligned well with the corresponding helices of the archaeal rhodopsins. **FIG. 5** also shows the amino acid residues that form a retinal binding pocket indicated by **520**. Although the proteorhodopsin proteins shown in **FIGS. 4** and **5** both originate from BAC31A8, they differ with respect to the second amino acid position. The reason is that the proteorhodopsin-specific PCR primers that were used to amplify the proteorhodopsin gene from BAC31A8 (which resulted in proteorhodopsin protein as in **FIG. 4**; **Sequence ID No:5**) included the addition of 3 nucleotides. These 3 nucleotides encoded one amino acid not found in the native gene sequence (**Sequence ID No:6**), in the second amino acid position which is a glycine located on the 2nd codon ("GGT"). Proteorhodopsin protein (**Sequence ID No:7**) as shown in **FIG. 5** originates from the native gene sequence without the addition of the 3 nucleotides. As mentioned above, the addition of the 3 nucleotides created a new restriction endonuclease site (NcoI site) that was not present in the native sequence and thereby allowed the amplified fragment to be subcloned into the NcoI site of the expression vector.

In the exemplary embodiment presented above, PCR primers with **Sequence ID No:2** and **Sequence ID No:3** were used. In general, the present invention provides a method for designing different proteorhodopsin-specific PCR primers that are all capable of amplifying a proteorhodopsin gene from DNA samples of naturally occurring microbial populations by polymerase chain reaction. In designing these

primers one first needs to determine a DNA sequence of a proteorhodopsin gene. Then one can design oligodeoxynucleotide primers with a Watson-Crick base pair complementary to 5' and 3' ends of the proteorhodopsin gene.

Variants of Proteorhodopsin

In the previous section, an exemplary embodiment is provided of a proteorhodopsin gene and protein. The present invention also provides the retrieval of genetic variations of proteorhodopsin from naturally occurring genetic variations in naturally occurring bacterial populations. These genetic variations in proteorhodopsin sequences result in functional variations in the proteorhodopsin proteins as is discussed below.

The present invention enables one skilled in the art to use the same proteorhodopsin-specific PCR primers as shown in FIGS. 2 and 3 to successfully amplify different sequence variants from DNA originating from mixed naturally occurring bacterial populations when it is compared to for instance the proteorhodopsin gene as shown in FIG. 4. As mentioned above, different proteorhodopsin-specific PCR primers could be used to amplify genetic variants of proteorhodopsin.

FIGS. 6-8 show exemplary embodiments of three different and unique variants of the proteorhodopsin gene that were retrieved from a recombinant DNA library of other naturally occurring bacteria (i.e. the bacterial artificial chromosome library (BAC)). In general, genetic variants could be obtained from different DNA libraries containing naturally occurring bacteria as well as from samples of naturally occurring bacteria. FIG. 6 shows the variant of the proteorhodopsin gene sequence (Sequence ID No:8) that is amplified from the BAC clone 40 (BAC40E8) with the same proteorhodopsin-

specific PCR primers as provided in **Sequence ID No:2** and **3**. Accordingly, **FIG. 6** also shows the deduced amino acid sequence (**Sequence ID No:9**) of the genetic variant of proteorhodopsin shown in **FIG. 6**. **FIG. 7** shows the variant of the proteorhodopsin gene sequence (**Sequence ID No:10**) that is amplified from the BAC clone 41 (BAC41B4) with the same proteorhodopsin-specific PCR primers as provided in **Sequence ID No:2** and **3**. Accordingly, **FIG. 7** also shows the deduced amino acid sequence (**Sequence ID No:11**) of the genetic variant of proteorhodopsin shown in **FIG. 7**. **FIG. 8** shows the variant of the proteorhodopsin gene sequence (**Sequence ID No:12**) that is amplified from the BAC clone 64 (BAC64A5) with the same proteorhodopsin-specific PCR primers as provided in **Sequence ID No:2** and **3**. Accordingly, **FIG. 8** also shows the deduced amino acid sequence (**Sequence ID No:13**) of the genetic variant of proteorhodopsin shown in **FIG. 8**.

FIG. 9 provides a variants map of the nucleotide sequences of the proteorhodopsin gene **Sequence ID No:4**, **Sequence ID No:8**, **Sequence ID No:10**, and **Sequence ID No:12** amplified from respectively BAC31A8, BAC40E8, BAC41B4 and BAC64A5 using the proteorhodopsin-specific PCR primers **Sequence ID No:2** and **Sequence ID No:3**. In **FIG. 9** lower case letters represent the PCR primer sequence region. Dots represent residues having identical sequence as those in **Sequence ID No:4**. These proteorhodopsin gene sequences differ by as much as 31 nucleotides as is shown in **FIG. 10**. **FIG. 10** provides a variant map of the deduced amino acid sequences of the proteorhodopsin genes shown in **FIG. 9**.

Using the same proteorhodopsin-specific PCR primers, as for instance shown in **FIGS. 2** and **3**, proteorhodopsin genes were also amplified from bacterioplankton extracts. As mentioned above, any proteorhodopsin-specific PCR primer can be used. These bacterioplankton extracts include those from the Monterey Bay (referred to as MB

clones), the Southern Ocean (Palmer Station, referred to as PAL clones), and waters of the central North Pacific Ocean (Hawaii Ocean Time series station, referred to as HOT clones).

FIGS. 11-36 show exemplary embodiments of different and unique variants of proteorhodopsin that were retrieved from the MB clones, PAL clones, and HOT clones. **FIGS. 11-36** each show a variant of a proteorhodopsin gene sequence that is amplified with the same proteorhodopsin-specific PCR primers as provided in **Sequence ID No:2** and **Sequence ID No:3** from respectively clones HOT0m1, HOT75m1, HOT75m3, HOT75m4, HOT75m8, MB0m1, MB0m2, MB20m2, MB20m5, MB20m12, MB40m1, MB40m5, MB40m12, MB100m5, MB100m7, MB100m9, MB100m10, PALB1, PALB2, PALB5, PALB7, PALB6, PALB8, PALE1, PALE6 and PALE7. The proteorhodopsin gene sequences retrieved from clones HOT0m1, HOT75m1, HOT75m3, HOT75m4, HOT75m8, MB0m1, MB0m2, MB20m2, MB20m5, MB20m12, MB40m1, MB40m5, MB40m12, MB100m5, MB100m7, MB100m9, MB100m10, PALB1, PALB2, PALB5, PALB7, PALB6, PALB8, PALE1, PALE6 and PALE7, have respectively **Sequence ID Nos: 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, and 64**. Accordingly, **FIGS. 11-36** also show the deduced amino acid sequence of each genetic variant of proteorhodopsin. The deduced amino acid sequence encoded by the proteorhodopsin gene retrieved from clones HOT0m1, HOT75m1, HOT75m3, HOT75m4, HOT75m8, MB0m1, MB0m2, MB20m2, MB20m5, MB20m12, MB40m1, MB40m5, MB40m12, MB100m5, MB100m7, MB100m9, MB100m10, PALB1, PALB2, PALB5, PALB7, PALB6, PALB8, PALE1, PALE6 and PALE7, have respectively **Sequence ID Nos: 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, and 65**.

In an exemplary embodiment shown in **FIG. 37**, fifteen different variants of proteorhodopsin in the PCR generated MB gene library **3710** were detected, falling into three clusters. The MB gene library includes MB clones MB0m2, MB40m5, MB20m2, MB40m12, MB100m10, MB20m12, MB40m1, MB100m5, MB20m5, MB100m7, MB0m1, and MB100m9 as well as BAC clones BAC40E8, BAC31A8 and BAC64A5. **FIG. 37** is based on a phylogenetic analysis of the inferred amino acids of cloned proteorhodopsin genes. Evolutionary distances calculated from 220 positions were used to infer the tree topology by the neighbor joining method using the PaupSearch program of the Wisconsin Package version 10.0 (Genetics Computer Group (GCG), Madison Wisconsin). Other methods could also be used. The variants of the MB library share at least 97% identity over 248 amino acids, as shown in **FIG. 38**, and 93% identity at the DNA level. All the PCR amplified proteorhodopsin genes from Antarctic marine bacterioplankton (e.g. the PAL clones) were different from those of Monterey Bay (e.g. the MB clones) sharing 78% identity over 248 amino acids with the Monterey clade. The changes in amino acid sequences were not restricted to the hydrophilic loops, but spread over the entire protein including changes near the retinal binding domain **3830** as shown in **FIG. 38**, which are predicted retinal-binding residues. **FIG. 38** shows an example of a multiple alignment of proteorhodopsin amino acid sequences that were obtained from different clones **3820**. The secondary structure is derived from hydropathy plots (boxes **3810** shows trans-membrane helices).

Light-driven energy generator

FIG. 39 provides a light-driven energy generator **3900** that utilizes proteorhodopsin, as obtained from naturally occurring bacteria as described above, to convert light-energy into biochemical energy. Light-driven energy generator **3900** takes advantage of the

functional properties of the proteorhodopsin protein once expressed in, for instance, *E. coli* and other bacteria. These properties include the ability of proteorhodopsin 3906 to integrate within the cell membrane 3904 of, for instance, *E. coli* making an integrated proteorhodopsin protein 3908 (also called an integrated cell membrane protein). These properties also include the ability of proteorhodopsin 3906 to bind retinal 3910, making a light absorbing pigment 3912. The source of retinal 3910 is not limited to chromophore retinal but could also include chemical derivatives of retinal, such as 3-methyl-5-(1-pyryl)-2E,4E-pentadienal, 3,7-dimethyl-9-(1-pyryl)-2E,4E,6E,8E-nonatetraenal, all-trans-9-(4-azido-2,3,5,6-tetrafluorophenyl)-3,7-dimethyl-2,4,6,8,-nonatetraenal and 2,3-dehydro-4-oxoretinal. Illuminating light absorbing pigment 3912 with a light source 3914 results in a chemiosmotic gradient or proton pump in which light energy 3916 is converted into biochemical energy 3918. The chemiosmotic gradient involves pumping of protons from the inside to the outside of cell membrane 3904. When the protons return to the inside of cell membrane 3904 it produces biochemical energy 3918 via a proton translocating ATP-ase. Finally, the biochemical energy 3918 is harnessed by a mediator 3920 to produce energy 3922 for a particular process. For example, since proteorhodopsin functions as a light driven proton pump, it generates energy in the form of a proton motive force across the host cell membrane upon illumination. This light-driven proton motive force can be converted to many other forms of energy, one example above being the regeneration of adenosine triphosphate (ATP), via a proton-translocating ATPase. This coupling of the proton motive force generated by proteorhodopsin, for use by proton-translocating ATPases to synthesize ATP, could be accomplished both in living cells, as well as in artificially constructed membrane systems such as liposomes. Proteorhodopsin-based systems can convert light energy to a wide variety of useful mechanical, chemical, and electrical energy forms, for many industrial and technological applications. These

include, but are not limited to, use in targeted drug delivery, uses as primary or secondary energy generators for biocatalytic reactors, fuel cells and nano-machines (including molecular motors), as well as uses in molecular switching or data storage devices.

Applications that can potentially benefit from proteorhodopsin-light driven energy generation are, for instance, bio-electronics applications that are aimed to interface, integrate, or substitute the silicon based microelectronics systems as well as molecular devices. Other applications that can potentially benefit from proteorhodopsin-light driven energy generation are, for instance, in bio-materials, wherein proteorhodopsin is integrated as a bio-material in, for instance, optical films for light mediated computer memory applications, optical information storage and pattern recognition.

Alternatively, proteorhodopsin is useful for a process to enhance yield or increase the potential of recombinant protein production or converting the light induced membrane potential into cellular signals, including modulation of gene expression. The biochemical energy derived from functional proteorhodopsin exposed to light could be harnessed to support a variety of cellular processes. For instance, the energy derived from light-mediated proton pumping could be used to enhance the production of secondary metabolites, or recombinant proteins in host cells, such as *E. coli*. Often, production of specific compounds in the biotechnology industry is limited, since their optimal expression or production occurs in the late stationary phase of growth, when energy reserves of the host cells are low. Retinal-bound proteorhodopsin expressed in such cells would provide an ample source of biochemical energy, by simple illumination. Proteorhodopsin-mediated light driven proton production could enhance any variety of biosynthetic or physiological processes which require energy.

The biochemical energy derived from proteorhodopsin light driven proton pumping could also be converted to other generally useful energy forms, for example electricity. Microbial fuel cells currently use carbon-based compounds, such as glucose, as the primary energy source. Via specific mediators of reduction potential (e.g. electrons), these microbial fuel cells convert cellular biochemical energy to electrical potential. Unlike carbon-based microbial fuel cells, proteorhodopsin uses light as the energy source, that can then be converted into a chemiosmotic potential, and finally into cellular biochemical energy by membrane-bound proton ATP-ases. Therefore, the use of proteorhodopsin could be employed to derive energy from light as the primary or supplementary energy source, that could then be converted into electrical potential (analogous microbial fuel cells that derive their energy from glucose).

In addition to energy generation in vivo in living cells, membranes containing proteorhodopsin could be used to enhance or enable other specific processes in vitro. Polymers produced from proteorhodopsin-containing membranes may have specific properties that could be used similarly to those containing bacteriorhodopsin. One example includes the use of these light sensitive molecules for optical computing applications.

As shown in FIG. 39, the kinetics of proteorhodopsin as it is utilized in 3900 is influenced by various factors such as the type of light source 3914 and the manipulation of light source 3914 in terms of frequency and/or wavelength at which the light 3916 is delivered. Light source 3914 could be any type of light source that delivers light energy 3916 that would be absorbed by light absorbing pigment 3918.

For example, the light source **3914** could be tuned to optimally excite rhodopsin variances with an absorbance maximum of 490 nm or alternatively those rhodopsins with an absorbance maximum of 520 nm. Manipulation of the light source **3914** or the light **3916** being emitted by the light source **3914**, for example, involves changing the frequency of fast-light pulses or the delivery of light **3916** as individual pulses, a train of pulses, or a continuous source of light. Manipulation also involves changing the wavelength of the delivery of light **3916** at different wavelengths. In addition, as is clear for one skilled in the art, changing the frequency and/or amount of retinal that will bind within integrated cell membrane protein **3908** also varies the function of proteorhodopsin. Finally, as was mentioned in the previous section, genetic variants of proteorhodopsin result in variants of the proteorhodopsin proteins that changes the kinetics of **3600** due to a difference in absorption of light at different wavelengths. The functional expression of such variation in these proteorhodopsin proteins adds another source of variation to the kinetics of proteorhodopsin as it is utilized in **3900**.

As shown in **FIG. 39**, the light-driven energy generator includes a host **3902**. In the present invention, as a preferred embodiment, host **3902** is a cell membrane preparation of *E. coli*. However, the present invention is not limited to the use of *E. coli* and, alternatively, other bacteria or eukaryotes could be used to provide host **3902** as an intact cell (in vivo) and/or as a cell membrane preparation (in vitro). For example, but not limited to, bacteria and yeast with developed genetic systems such as *Bacillus* spp. Species, *Saccharomyces* spp., *Streptomyces* spp. or *Pichia* spp. could be used as host for the expression of proteorhodopsin. In addition, in case a cell membrane preparation (in vitro) is used, host **3902** becomes equivalent to cell membrane **3904**.

The light-driven energy generator **3900**, as shown in **FIG. 39**, further includes proteorhodopsin **3906**. Proteorhodopsin is presented in the form of the earlier presented expression vector containing a proteorhodopsin gene or one of its variants. Once proteorhodopsin **3906** has been put into host **3902**, the proteorhodopsin expression vector expresses the proteorhodopsin protein in host **3902**. An integral cell membrane protein **3908** is created in which the proteorhodopsin protein inserts into and folds properly within the cell membrane **3904**. This is accomplished in the *E. coli* host by virtue of the native signal sequence found in the 5' end of the proteorhodopsin gene. It could also be accomplished by replacement of native sequence with another host-specific signal sequence in non-*E. coli* host systems.

As shown in **FIG. 39**, once retinal **3910** is added to cell membrane **3904**, retinal **3910** binds within integrated cell membrane protein **3908** and forms a light absorbing pigment **3912**. The particular example of **FIG. 40** shows an integrated proteorhodopsin protein **3908** bound to retinal **3910** in *E. coli*. Chemical derivatives of retinal (as discussed above) could also be used as a substitute chromophore to generate functional proteorhodopsin. For the particular example of **FIG. 40**, the proteorhodopsin protein was cloned with its native signal sequence and included an addition of the V5 epitope, and a polyhistidine tail in the C-terminus. The proteorhodopsin protein was expressed in host **3902**, i.e. *E. coli* outer-membrane protease-deficient strain UT5600, and induced with 0.2 % arabinose for 3 hours. Cell membranes **3904** were prepared and resuspended in 50 mM Tris-Cl (pH 8.0) and 5 mM MgCl₂. **FIG. 40** shows a proteorhodopsin-expressing *E. coli* cell suspension. After 3 hours of induction in the presence of 10 µM all-trans retinal, cells expressing the protein acquire a reddish pigmentation as indicated by **4010** and the + (plus) symbol. **FIG. 40** also shows that a cell suspension using the same PCR primers

(Sequence ID No:2 and 3) but now in opposite orientation as a negative control, did not acquire a reddish pigmentation as indicated by 4020 and the – (minus) symbol.

FIG. 41 shows an exemplary embodiment of the absorption spectra of light absorbing pigment 3912 upon illumination with light source 3914 as is shown in **FIG. 39**. As mentioned above, the light absorbing pigment is a retinal-reconstituted proteorhodopsin in *E. coli*. **FIG. 41** shows absorption spectra of light absorbing pigment 3912 as well as a negative control. After retinal 3910 addition to integrated proteorhodopsin protein 3908, light absorbing pigment 3912 was made. The retinal 3910 addition was done at selected time points, i.e. 10, 20, 30 and 40 min, and shows a progression from low to high absorption values indicated by respectively 4110, 4120, 4130 and 4140 upon illumination with light source 3914. **FIG. 41** also shows the absorption spectra of retinal 3910 addition at these similar time points but now to a negative control of retinal 3910 containing a proteorhodopsin 3906 that was created using the same PCR primers in opposite orientation. 4150, 4160, 4170 and 4180 indicate the four absorption spectra for the negative control. An absorption peak at 520 nm was observed after 10 minutes (4110) of incubation as illustrated in **FIG. 41**. On further addition of retinal, the peak at 520 nm increased, and had a ~100 nm half bandwidth. The 520 nm absorption peak was generated only in membranes containing proteorhodopsin 3906, and only in the presence of retinal 3910. The red shifted λ_{max} of retinal ($\lambda_{\text{max}} = 370$ nm in the free state) is indicative of a protonated Schiff base covalent linkage of retinal to proteorhodopsin.

FIG. 42 shows an exemplary embodiment of the light mediated proton pump of the light-driven energy generator 3900 indicating the conversion of light energy 3916 as shown in **FIG. 39**. The proton pump action is illustrated by measuring pH changes in

the medium surrounding the host 3902, which in this particular example involves a cell suspension of *E. coli*, illuminated by light source 3914. The beginning and cessation of illumination (with yellow light >485 nm delivered by 3916) is indicated 4110 ("ON") and 4120 ("OFF") respectively. The cells were suspended in 10 mM NaCl, 10 mM $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ and 100 μM CaCl_2 . Net outward transport of protons was observed solely in proteorhodopsin-containing *E. coli* cells, and only in the presence of retinal 3910 and light 3916 and is indicated by 4210 in FIG. 42. Light-induced acidification of the medium was completely abolished by the presence of 10 μM of the protonophore CCCP.

FIG. 43 is an exemplary embodiment showing that illumination by light source 3914 generates an electrical potential at the membrane 3904 in proteorhodopsin-containing right-side-out membrane vesicles, in the presence of retinal 3910, reaching -90 mV after 2 minutes from light 3916 onset. Transport of $[^3\text{H}]\text{TPP}^+$ in *E. coli* right-side-out vesicles containing expressed proteorhodopsin, reconstituted with (4310 and 4320) or without (4330 and 4340) 10 μM retinal 3910 in the presence of light (4310 and 4330) delivered by the light source 3914 or in the dark (4320 and 4340). FIG. 43 shows that proteorhodopsin, in its form of 3912 as a light absorbing pigment, pumps protons from the inside to the outside of cell membrane in a physiologically relevant range. The ability of proteorhodopsin to generate a physiologically significant membrane potential, even when heterologously expressed in nonnative membranes, is consistent with the proton pumping function for proteorhodopsin in the native gamma proteobacteria from which it is derived.

FIG. 44 is an exemplary embodiment showing that proteorhodopsin can have a fast photocycle and can therefore be characterized as a fast and therefore efficient

transporter of protons. For the particular example of FIG. 44, light absorbing pigment 3912 is induced by laser pulses delivered by light source 3914. Laser pulse-induced absorption changes are shown by 3912 in host 3902, which in this case are suspensions of *E. coli* membranes containing proteorhodopsin. A 532-nm pulse (6 ns duration, 40 mJ) was delivered at time 0 and absorption changes were monitored at various wavelengths in the visible range in a lab-constructed pulse photolysis system. 64 transients were collected for each wavelength. 4410 indicates transients at 3 wavelengths exhibiting maximal amplitudes. 4420 indicates absorption difference spectra calculated from amplitudes at 0.5 ms (indicated by 4430) and between 0.5 ms and 5.0 ms (indicated by 4440). In 4410, transient depletion occurred near the absorption maximum of pigment 3912 (500-nm trace indicated by 4450), and transient absorption increase was detected at 400 nm (indicated by 4460) and 590 nm (indicated by 4470), indicating a functional photocyclic reaction pathway. In 4420, the absorption difference spectrum shows that within 0.5 ms an intermediate with maximal absorption near 400 nm is produced (indicated by 4430), typical of unprotonated Schiff base forms (M intermediates) of retinylidene pigments. The 5-ms minus 0.5-ms difference spectrum 4440 shows that following M decay an intermediate species red-shifted from the unphotolyzed 520-nm state appears. The decay of proteorhodopsin final intermediate is the rate limiting step in the photocycle and is fit well by a single exponential process of 15 ms, with an upward baseline shift of 13% of the initial amplitude.

As mentioned above, a proteorhodopsin gene or protein variant can be selected to determine an absorption spectra of the light absorbing pigment to change the kinetics of the light energy generator 3900, for instance to meet a design/functional criteria of an application wherein proteorhodopsin is utilized. FIG. 45 shows an exemplary

embodiment of different absorption spectra of retinal-reconstituted proteorhodopsins in *E. coli* as a function of wavelength 4510. As shown in FIG. 45, the absorbance 4520 is different and depends on the clone from which the proteorhodopsin was amplified. In this particular example, 5 μ m all-*trans* retinal was added to the membranes suspensions in a 100 mM phosphate buffer, with a pH 7.0, and absorption spectra were recorded. The four spectra 4530, 4540, 4550, and 4560 are respectively for the proteorhodopsin genes retrieved from clones HOT75m4, PALE6, HOT0m1, and BAC31A8 at 1 hour after retinal addition. The proteorhodopsin gene retrieved from clone HOT75m4 4530 and PALE6 4540 produced a blue (490 nm) absorption maximum. The proteorhodopsin gene retrieved from clone HOT0m1 4550 and BAC31A8 4560 produced a green (527 nm) absorption maximum. In general, a range of wavelengths could be obtained that is not limited to the range shown in the example of FIG. 45.

It will be clear to one skilled in the art that the above embodiment may be altered in many ways without departing from the scope of the invention, such as for instance by mutagenesis to change the genetic sequence of proteorhodopsin and thereby changing the kinetics of the proteorhodopsin protein once it is expressed. Accordingly, the following claims and their legal equivalents should determine the scope of the invention.

DEPOSITS

Depository address: 10801 University Boulevard, Manassas, VA 20110, USA.

The *Escherichia coli* containing cloned DNA BAC 31A8 having assigned ATCC number PTA-3083, the *Escherichia coli* containing cloned DNA BAC 40E8 having assigned ATCC number PTA-3082, the *Escherichia coli* containing cloned DNA BAC 41B4 having assigned ATCC number PTA-3080, and the *Escherichia coli* containing cloned DNA BAC 64A5 having assigned ATCC number PTA-3081, all having been deposited on February 21, 2001 with the ATCC Patent Depository.

The *Escherichia coli* containing a plasmid PAL E6 having assigned ATCC number PTA-3250, the *Escherichia coli* containing a plasmid HOT 0m1 having assigned ATCC number PTA-3251, the *Escherichia coli* containing a plasmid HOT 75m4 having assigned ATCC number PTA-3252, and the *Escherichia coli* containing cloned DNA BAC64A5 having assigned ATCC number PTA 3082, all having been deposited on March 30, 2001 with the ATCC Patent Depository.

LIGHT-DRIVEN ENERGY GENERATION USING
PROTEORHODOPSIN

LIST OF SEQUENCES THAT ARE LISTED IN THE
INCORPORATED SEQUENCE LISTING

- Sequence ID No:1** bacterial artificial chromosome (BAC) clone 31A8 (EBAC31A8).
- Sequence ID No:2** nucleotide sequence of proteorhodopsin-specific polymerase chain reaction (PCR) primer 1.
- Sequence ID No:3** nucleotide sequence of proteorhodopsin-specific polymerase chain reaction (PCR) primer 2.
- Sequence ID No:4** nucleotide sequence of the proteorhodopsin gene amplified from clone EBAC31A8 (Sequence ID No. 1) using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:5** deduced amino acid sequences of the proteorhodopsin gene amplified from clone EBAC31A8 (Sequence ID NO:4).
- Sequence ID No:6** native proteorhodopsin nucleotide sequence from clone EBAC31A8 (Sequence ID No:1).

- Sequence ID No:7** deduced amino acid sequences of the native proteorhodopsin nucleotide sequence from clone EBAC31A8 (Sequence ID No:6).
- Sequence ID No:8** nucleotide sequence of the proteorhodopsin gene amplified from clone EBAC40E8 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:9** deduced amino acid sequences of the proteorhodopsin gene amplified from clone EBAC40E8 (Sequence ID NO:8).
- Sequence ID No:10** nucleotide sequence of the proteorhodopsin gene amplified from clone EBAC41B4 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:11** deduced amino acid sequences of the proteorhodopsin gene amplified from clone EBAC41B4 (Sequence ID NO:10).
- Sequence ID No:12** nucleotide sequence of the proteorhodopsin gene amplified from clone EBAC64A5 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:13** deduced amino acid sequences of the proteorhodopsin gene amplified from clone EBAC64A5 (Sequence ID NO:12).

- Sequence ID No:14** nucleotide sequence of the proteorhodopsin gene amplified from clone HOT0m1 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:15** deduced amino acid sequences of the proteorhodopsin gene amplified from clone HOT0m1 (Sequence ID NO:14).
- Sequence ID No:16** nucleotide sequence of the proteorhodopsin gene amplified from clone HOT75m1 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:17** deduced amino acid sequences of the proteorhodopsin gene amplified from clone HOT75m1 (Sequence ID NO:16).
- Sequence ID No:18** nucleotide sequence of the proteorhodopsin gene amplified from clone HOT75m3 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:19** deduced amino acid sequences of the proteorhodopsin gene amplified from clone HOT75m3 (Sequence ID NO:18).
- Sequence ID No:20** nucleotide sequence of the proteorhodopsin gene amplified from clone HOT75m4 using PCR primers according to Sequence ID No:2 and Sequence No:3.

- Sequence ID No:21** deduced amino acid sequences of the proteorhodopsin gene amplified from clone HOT75m4 (Sequence ID NO:20).
- Sequence ID No:22** nucleotide sequence of the proteorhodopsin gene amplified from clone HOT75m8 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:23** deduced amino acid sequences of the proteorhodopsin gene amplified from clone HOT75m8 (Sequence ID NO:22).
- Sequence ID No:24** nucleotide sequence of the proteorhodopsin gene amplified from clone MB0m1 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:25** deduced amino acid sequences of the proteorhodopsin gene amplified from clone MB0m1 (Sequence ID NO:24).
- Sequence ID No:26** nucleotide sequence of the proteorhodopsin gene amplified from clone MB0m2 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:27** deduced amino acid sequences of the proteorhodopsin gene amplified from clone MB0m2 (Sequence ID NO:26).

- Sequence ID No:28** nucleotide sequence of the proteorhodopsin gene amplified from clone MB20m2 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:29** deduced amino acid sequences of the proteorhodopsin gene amplified from clone MB20m2 (Sequence ID NO:28).
- Sequence ID No:30** nucleotide sequence of the proteorhodopsin gene amplified from clone MB20m5 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:31** deduced amino acid sequences of the proteorhodopsin gene amplified from clone MB20m5 (Sequence ID NO:30).
- Sequence ID No:32** nucleotide sequence of the proteorhodopsin gene amplified from clone MB20m12 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:33** deduced amino acid sequences of the proteorhodopsin gene amplified from clone MB20m12 (Sequence ID NO:32).
- Sequence ID No:34** nucleotide sequence of the proteorhodopsin gene amplified from clone MB40m1 using PCR primers according to Sequence ID No:2 and Sequence No:3.

- Sequence ID No:35** deduced amino acid sequences of the proteorhodopsin gene amplified from clone MB40m1 (Sequence ID NO:34).
- Sequence ID No:36** nucleotide sequence of the proteorhodopsin gene amplified from clone MB40m5 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:37** deduced amino acid sequences of the proteorhodopsin gene amplified from clone MB40m5 (Sequence ID NO:36).
- Sequence ID No:38** nucleotide sequence of the proteorhodopsin gene amplified from clone MB40m12 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:39** deduced amino acid sequences of the proteorhodopsin gene amplified from clone MB40m12 (Sequence ID NO:38).
- Sequence ID No:40** nucleotide sequence of the proteorhodopsin gene amplified from clone MB100m5 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:41** deduced amino acid sequences of the proteorhodopsin gene amplified from clone MB100m5 (Sequence ID NO:40).

- Sequence ID No:42** nucleotide sequence of the proteorhodopsin gene amplified from clone MB100m7 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:43** deduced amino acid sequences of the proteorhodopsin gene amplified from clone MB100m7 (Sequence ID NO:42).
- Sequence ID No:44** nucleotide sequence of the proteorhodopsin gene amplified from clone MB100m9 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:45** deduced amino acid sequences of the proteorhodopsin gene amplified from clone MB100m9 (Sequence ID NO:44).
- Sequence ID No:46** nucleotide sequence of the proteorhodopsin gene amplified from clone MB100m10 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:47** deduced amino acid sequences of the proteorhodopsin gene amplified from clone MB100m10 (Sequence ID NO:46).
- Sequence ID No:48** nucleotide sequence of the proteorhodopsin gene amplified from clone PALB1 using PCR primers according to Sequence ID No:2 and Sequence No:3.

- Sequence ID No:49** deduced amino acid sequences of the proteorhodopsin gene amplified from clone PALB1 (Sequence ID NO:48).
- Sequence ID No:50** nucleotide sequence of the proteorhodopsin gene amplified from clone PALB2 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:51** deduced amino acid sequences of the proteorhodopsin gene amplified from clone PALB2 (Sequence ID NO:50).
- Sequence ID No:52** nucleotide sequence of the proteorhodopsin gene amplified from clone PALB5 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:53** deduced amino acid sequences of the proteorhodopsin gene amplified from clone PALB5 (Sequence ID NO:52).
- Sequence ID No:54** nucleotide sequence of the proteorhodopsin gene amplified from clone PALB7 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:55** deduced amino acid sequences of the proteorhodopsin gene amplified from clone PALB7 (Sequence ID NO:54).

- Sequence ID No:56** nucleotide sequence of the proteorhodopsin gene amplified from clone PALB6 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:57** deduced amino acid sequences of the proteorhodopsin gene amplified from clone PALB6 (Sequence ID NO:56).
- Sequence ID No:58** nucleotide sequence of the proteorhodopsin gene amplified from clone PALB8 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:59** deduced amino acid sequences of the proteorhodopsin gene amplified from clone PALB8 (Sequence ID NO:58).
- Sequence ID No:60** nucleotide sequence of the proteorhodopsin gene amplified from clone PALE1 using PCR primers according to Sequence ID No:2 and Sequence No:3.
- Sequence ID No:61** deduced amino acid sequences of the proteorhodopsin gene amplified from clone PALE1 (Sequence ID NO:60).
- Sequence ID No:62** nucleotide sequence of the proteorhodopsin gene amplified from clone PALE6 using PCR primers according to Sequence ID No:2 and Sequence No:3.

Sequence ID No:63 deduced amino acid sequences of the proteorhodopsin gene amplified from clone PALE6 (Sequence ID NO:62).

Sequence ID No:64 nucleotide sequence of the proteorhodopsin gene amplified from clone PALE7 using PCR primers according to Sequence ID No:2 and Sequence No:3.

Sequence ID No:65 deduced amino acid sequences of the proteorhodopsin gene amplified from clone PALE7 (Sequence ID NO:64).

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CLAIMS

What is claimed is:

1. A proteorhodopsin gene, comprising an isolated DNA sequence for encoding a proteorhodopsin protein.
2. The proteorhodopsin gene of claim 1, wherein said proteorhodopsin gene is retrieved from a genomic fragment of a sample of naturally occurring bacteria.
3. The proteorhodopsin gene of claim 2, wherein said naturally occurring bacteria are marine proteobacteria.
4. The proteorhodopsin gene of claim 2, wherein said naturally occurring bacteria are SAR86 bacteria.
5. The proteorhodopsin gene of claim 2, wherein said naturally occurring bacterial genomic fragment is retrieved from a recombinant DNA library.
6. The proteorhodopsin gene of claim 5, wherein said naturally occurring bacterial genomic fragment is retrieved from a bacterial artificial chromosome library.

7. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone BAC31A8, said proteorhodopsin gene is Sequence ID No:4 and said proteorhodopsin protein is Sequence ID No:5.
8. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone BAC40E8, said proteorhodopsin gene is Sequence ID No:8 and said proteorhodopsin protein is Sequence ID No:9.
9. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone BAC41B4, said proteorhodopsin gene is Sequence ID No:10 and said proteorhodopsin protein is Sequence ID No:11.
10. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone BAC64A5, said proteorhodopsin gene is Sequence ID No:12 and said proteorhodopsin protein is Sequence ID No:13.
11. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone HOT0m1, said proteorhodopsin gene is Sequence ID No:14 and said proteorhodopsin protein is Sequence ID No:15.

12. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone HOT75m1, said proteorhodopsin gene is Sequence ID No:16 and said proteorhodopsin protein is Sequence ID No:17.
13. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone HOT75m3, said proteorhodopsin gene is Sequence ID No:18 and said proteorhodopsin protein is Sequence ID No:19.
14. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone HOT75m4, said proteorhodopsin gene is Sequence ID No:20 and said proteorhodopsin protein is Sequence ID No:21.
15. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone HOT75m8, said proteorhodopsin gene is Sequence ID No:22 and said proteorhodopsin protein is Sequence ID No:23.
16. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone MB0m1, said proteorhodopsin gene is Sequence ID No:24 and said proteorhodopsin protein is Sequence ID No:25.

17. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone MB0m2, said proteorhodopsin gene is Sequence ID No:26 and said proteorhodopsin protein is Sequence ID No:27.
18. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone MB20m2, said proteorhodopsin gene is Sequence ID No:28 and said proteorhodopsin protein is Sequence ID No:29.
19. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone MB20m5, said proteorhodopsin gene is Sequence ID No:30 and said proteorhodopsin protein is Sequence ID No:31.
20. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone MB20m12, said proteorhodopsin gene is Sequence ID No:32 and said proteorhodopsin protein is Sequence ID No:33.
21. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone MB40m1, said proteorhodopsin gene is Sequence ID No:34 and said proteorhodopsin protein is Sequence ID No:35.

22. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone MB40m5, said proteorhodopsin gene is Sequence ID No:36 and said proteorhodopsin protein is Sequence ID No:37.
23. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone MB40m12, said proteorhodopsin gene is Sequence ID No:38 and said proteorhodopsin protein is Sequence ID No:39.
24. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone MB100m5, said proteorhodopsin gene is Sequence ID No:40 and said proteorhodopsin protein is Sequence ID No:41.
25. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone MB100m7, said proteorhodopsin gene is Sequence ID No:42 and said proteorhodopsin protein is Sequence ID No:43.
26. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone MB100m9, said proteorhodopsin gene is Sequence ID No:44 and said proteorhodopsin protein is Sequence ID No:45.

27. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone MB100m10, said proteorhodopsin gene is Sequence ID No:46 and said proteorhodopsin protein is Sequence ID No:47.
28. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone PALB1, said proteorhodopsin gene is Sequence ID No:48 and said proteorhodopsin protein is Sequence ID No:49.
29. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone PALB2, said proteorhodopsin gene is Sequence ID No:50 and said proteorhodopsin protein is Sequence ID No:51.
30. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone PALB5, said proteorhodopsin gene is Sequence ID No:52 and said proteorhodopsin protein is Sequence ID No:53.
31. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone PALB7, said proteorhodopsin gene is Sequence ID No:54 and said proteorhodopsin protein is Sequence ID No:55.

32. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone PALB6, said proteorhodopsin gene is Sequence ID No:56 and said proteorhodopsin protein is Sequence ID No:57.
33. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone PALB8, said proteorhodopsin gene is Sequence ID No:58 and said proteorhodopsin protein is Sequence ID No:59.
34. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone PALE1, said proteorhodopsin gene is Sequence ID No:60 and said proteorhodopsin protein is Sequence ID No:61.
35. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone PALE6, said proteorhodopsin gene is Sequence ID No:62 and said proteorhodopsin protein is Sequence ID No:63.
36. The proteorhodopsin gene of claim 2, wherein said genomic fragment is retrieved from a clone PALE7, said proteorhodopsin gene is Sequence ID No:64 and said proteorhodopsin protein is Sequence ID No:65.

37. The proteorhodopsin gene of claim 1, wherein said proteorhodopsin gene is amplified from a genomic fragment by polymerase chain reaction.
38. The proteorhodopsin gene of claim 37, wherein said polymerase chain reaction is performed by primers with Sequence ID No:2 and Sequence ID No:3.
39. The proteorhodopsin gene of claim 1, wherein said proteorhodopsin gene is derived from a marine environment and placed in an expression vector for producing said proteorhodopsin protein in a host.
40. The proteorhodopsin gene of claim 39, wherein said host is an artificial membrane system.
41. The proteorhodopsin gene of claim 39, wherein said host is a bacterium.
42. The proteorhodopsin gene of claim 41, wherein said host is a cell membrane preparation of said bacterium.
43. The proteorhodopsin gene of claim 39, wherein said host is an eukaryote.
44. The proteorhodopsin gene of claim 43, wherein said host is a cell membrane preparation of said eukaryote.

45. A method of retrieving a proteorhodopsin gene, comprising the steps of:
- (a) providing a sample of naturally occurring bacteria;
 - (b) extracting a genomic fragment of said sample of naturally occurring bacteria; and
 - (c) amplifying said proteorhodopsin gene from said genomic fragment using polymerase chain reaction.
46. The method of claim 45, further comprising the step of creating an expression vector containing said proteorhodopsin gene.
47. The method of claim 45, wherein said naturally occurring bacteria are marine proteobacteria.
48. The method of claim 45, wherein said naturally occurring bacteria are SAR86 bacteria.
49. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is retrieved from a recombinant DNA library.
50. The method of claim 49, said naturally occurring bacterial genomic fragment is retrieved from a bacterial artificial chromosome library.
51. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone BAC31A8, and wherein said amplified

- proteorhodopsin gene from said clone BAC31A8 is Sequence ID No:4 and encodes a proteorhodopsin protein according to Sequence ID No:5.
52. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone BAC40E8, and wherein said amplified proteorhodopsin gene from said clone BAC40E8 is Sequence ID No:8 and encodes a proteorhodopsin protein according to Sequence ID No:9.
53. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone BAC41B4, and wherein said amplified proteorhodopsin gene from said clone BAC41B4 is Sequence ID No:10 and encodes a proteorhodopsin protein according to Sequence ID No:11.
54. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone BAC64A5, and wherein said amplified proteorhodopsin gene from said clone BAC64A5 is Sequence ID No:12 and encodes a proteorhodopsin protein according to Sequence ID No:13.
55. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone HOT0m1, and wherein said amplified proteorhodopsin gene from said clone HOT0m1 is Sequence ID No:14 and encodes a proteorhodopsin protein according to Sequence ID No:15.
56. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone HOT75m1, and wherein said amplified

proteorhodopsin gene from said clone HOT75m1 is Sequence ID No:16 and encodes a proteorhodopsin protein according to Sequence ID No:17.

57. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone HOT75m3, and wherein said amplified proteorhodopsin gene from said clone HOT75m3 is Sequence ID No:18 and encodes a proteorhodopsin protein according to Sequence ID No:19.
58. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone HOT75m4, and wherein said amplified proteorhodopsin gene from said clone HOT75m4 is Sequence ID No:20 and encodes a proteorhodopsin protein according to Sequence ID No:21.
59. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone HOT75m8, and wherein said amplified proteorhodopsin gene from said clone HOT75m8 is Sequence ID No:22 and encodes a proteorhodopsin protein according to Sequence ID No:23.
60. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone MB0m1, and wherein said amplified proteorhodopsin gene from said clone MB0m1 is Sequence ID No:24 and encodes a proteorhodopsin protein according to Sequence ID No:25.
61. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone MB0m2, and wherein said amplified

proteorhodopsin gene from said clone MB0m2 is Sequence ID No:26 and encodes a proteorhodopsin protein according to Sequence ID No:27.

62. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone MB20m2, and wherein said amplified proteorhodopsin gene from said clone MB20m2 is Sequence ID No:28 and encodes a proteorhodopsin protein according to Sequence ID No:29.
63. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone MB20m5, and wherein said amplified proteorhodopsin gene from said clone MB20m5 is Sequence ID No:30 and encodes a proteorhodopsin protein according to Sequence ID No:31.
64. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone MB20m12, and wherein said amplified proteorhodopsin gene from said clone MB20m12 is Sequence ID No:32 and encodes a proteorhodopsin protein according to Sequence ID No:33.
65. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone MB40m1, and wherein said amplified proteorhodopsin gene from said clone MB40m1 is Sequence ID No:34 and encodes a proteorhodopsin protein according to Sequence ID No:35.
66. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone MB40m5, and wherein said amplified

proteorhodopsin gene from said clone MB40m5 is Sequence ID No:36 and encodes a proteorhodopsin protein according to Sequence ID No:37.

67. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone MB40m12, and wherein said amplified proteorhodopsin gene from said clone MB40m12 is Sequence ID No:38 and encodes a proteorhodopsin protein according to Sequence ID No:39.

68. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone MB100m5, and wherein said amplified proteorhodopsin gene from said clone MB100m5 is Sequence ID No:40 and encodes a proteorhodopsin protein according to Sequence ID No:41.

69. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone MB100m7, and wherein said amplified proteorhodopsin gene from said clone MB100m7 is Sequence ID No:42 and encodes a proteorhodopsin protein according to Sequence ID No:43.

70. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone MB100m9, and wherein said amplified proteorhodopsin gene from said clone MB100m9 is Sequence ID No:44 and encodes a proteorhodopsin protein according to Sequence ID No:45.

71. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone MB100m10, and wherein said amplified

proteorhodopsin gene from said clone MB100m10 is Sequence ID No:46 and encodes a proteorhodopsin protein according to Sequence ID No:47.

72. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone PALB1, and wherein said amplified proteorhodopsin gene from said clone PALB1 is Sequence ID No:48 and encodes a proteorhodopsin protein according to Sequence ID No:49.
73. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone PALB2, and wherein said amplified proteorhodopsin gene from said clone PALB2 is Sequence ID No:50 and encodes a proteorhodopsin protein according to Sequence ID No:51.
74. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone PALB5, and wherein said amplified proteorhodopsin gene from said clone PALB5 is Sequence ID No:52 and encodes a proteorhodopsin protein according to Sequence ID No:53.
75. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone PALB7, and wherein said amplified proteorhodopsin gene from said clone PALB7 is Sequence ID No:54 and encodes a proteorhodopsin protein according to Sequence ID No:55.
76. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone PALB6, and wherein said amplified

proteorhodopsin gene from said clone PALB6 is Sequence ID No:56 and encodes a proteorhodopsin protein according to Sequence ID No:57.

77. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone PALB8, and wherein said amplified proteorhodopsin gene from said clone PALB8 is Sequence ID No:58 and encodes a proteorhodopsin protein according to Sequence ID No:59.
78. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone PALE1, and wherein said amplified proteorhodopsin gene from said clone PALE1 is Sequence ID No:60 and encodes a proteorhodopsin protein according to Sequence ID No:61.
79. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone PALE6, and wherein said amplified proteorhodopsin gene from said clone PALE6 is Sequence ID No:62 and encodes a proteorhodopsin protein according to Sequence ID No:63.
80. The method of claim 45, wherein said naturally occurring bacterial genomic fragment is in a clone PALE7, and wherein said amplified proteorhodopsin gene from said clone PALE7 is Sequence ID No:64 and encodes a proteorhodopsin protein according to Sequence ID No:65.
81. The method of claim 45, wherein said polymerase chain reaction is performed by primers with Sequence ID No:2 and Sequence ID No:3.

82. The method of claim 45, further comprising the step of providing a host.
83. The method of claim 82, wherein said host is an artificial membrane system.
84. The method of claim 82, wherein said host is a bacterium.
85. The method of claim 84, wherein said host is a cell membrane preparation of said bacterium.
86. The method of claim 82, wherein said host is an eukaryote.
87. The method of claim 86, wherein said host is a cell membrane preparation of said eukaryote.
88. A light-driven energy generator, comprising:
- (a) a proteorhodopsin protein;
 - (b) a host to correctly fold said proteorhodopsin protein in said host, thereby creating an integrated proteorhodopsin protein; and
 - (c) a source of retinal to bind covalently to said integrated proteorhodopsin protein, thereby creating a light absorbing pigment.
89. The light-driven energy generator of claim 88, wherein said proteorhodopsin protein is encoded by a proteorhodopsin gene retrieved from a genomic fragment of a sample of naturally occurring bacteria.

90. The light-driven energy generator of claim 89, wherein said naturally occurring bacteria are marine proteobacteria.
91. The light-driven energy generator of claim 89, wherein said naturally occurring bacteria are SAR86 bacteria.
92. The light-driven energy generator of claim 89, wherein said naturally occurring bacterial genomic fragment is retrieved from a recombinant DNA library.
93. The light-driven energy generator of claim 92, wherein said naturally occurring bacterial genomic fragment is retrieved from a bacterial artificial chromosome library.
94. The light-driven energy generator of claim 89, wherein said genomic fragment is retrieved from a clone, wherein said clone is a member of the group consisting of BAC31A8, BAC40E8, BAC41B4, BAC64A5, HOT0m1, HOT75m1, HOT75m3, HOT75m4, HOT75m8, MB0m1, MB0m2, MB20m2, MB20m5, MB20m12, MB40m1, MB40m5, MB40m12, MB100m5, MB100m7, MB100m9, MB100m10, PALB1, PALB2, PALB5, PALB7, PALB6, PALB8, PALE1, PALE6 and PALE7.
95. The light-driven energy generator of claim 88, wherein said host is an artificial membrane system.

96. The light-driven energy generator of claim 88, wherein said host is a cell membrane obtained from a bacterium.
97. The light-driven energy generator of claim 96, wherein said host is a cell membrane preparation obtained from a bacterium.
98. The light-driven energy generator of claim 88, wherein said host is a cell membrane obtained from an eukaryote.
99. The light-driven energy generator of claim 98, wherein said host is a cell membrane preparation obtained from an eukaryote.
100. The light-driven energy generator of claim 88, further comprising a light source for illuminating said light absorbing pigment, whereby said energy generator converts light into biochemical energy.
101. The light-driven energy generator of claim 100, wherein said light source is a fast-pulsed light source.
102. The light-driven energy generator of claim 101, wherein said fast-pulsed light source comprises a mechanism for delivering intermittent fast-light pulses at predetermined time intervals.

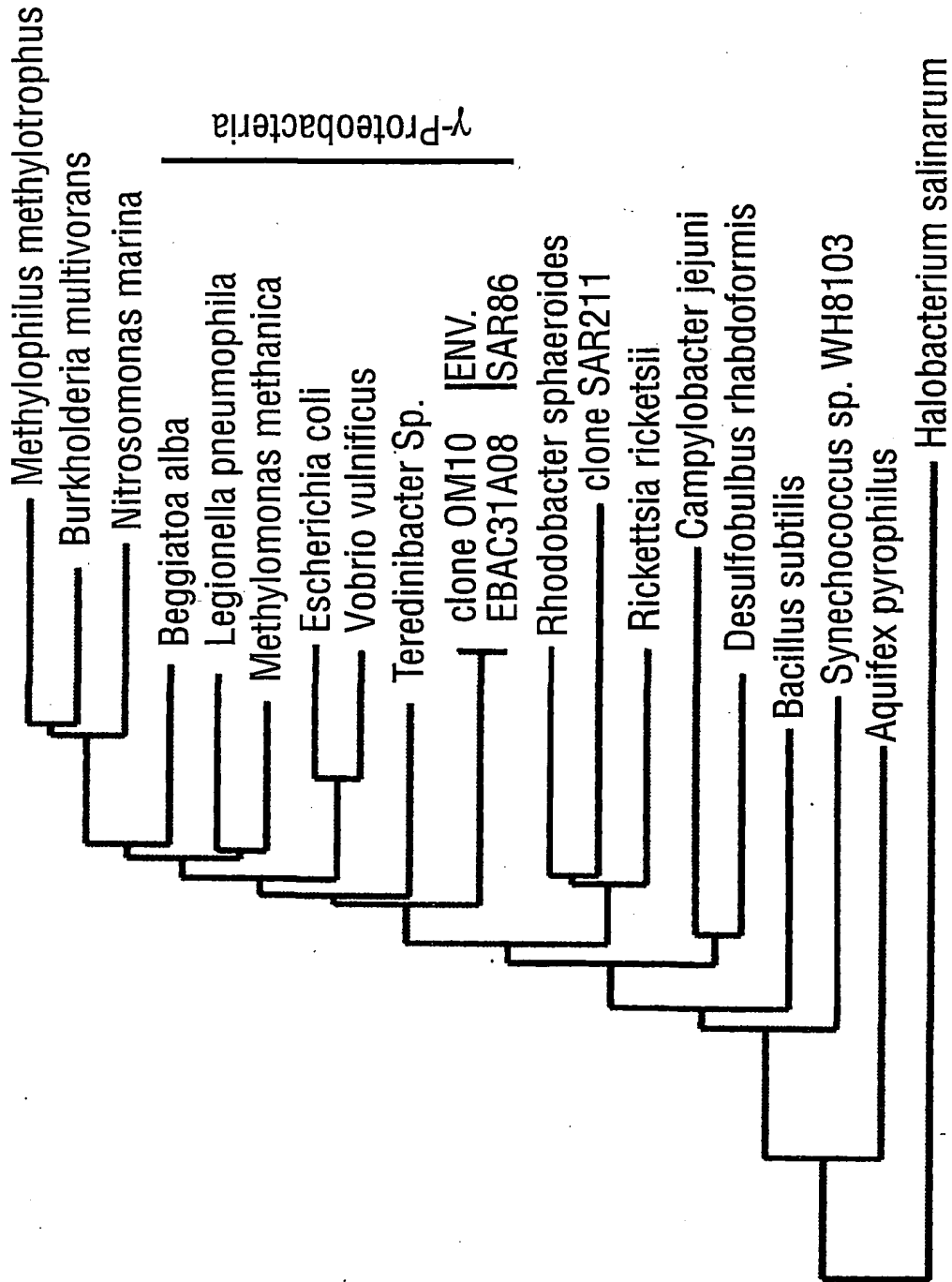
103. The light-driven energy generator of claim 100, wherein said light source is a light source exhibiting different predetermined wavelengths.
104. The light-driven energy generator of claim 88, further comprising a mediator for mediating energy generated by said energy generator into chemical, mechanical or electrical energy.
105. The light-driven energy generator of claim 88, wherein said proteorhodopsin protein is selected to determine an absorption spectra of said light absorbing pigment.
106. A method for making a light-driven energy generator, comprising the steps of:
- (a) providing a proteorhodopsin protein;
 - (b) providing a host to correctly fold said proteorhodopsin protein in said host, thereby creating an integrated proteorhodopsin protein; and
 - (c) providing a source of retinal to bind covalently to said integrated proteorhodopsin protein, thereby creating a light absorbing pigment.
107. The method of claim 106, wherein said proteorhodopsin protein is encoded by a proteorhodopsin gene retrieved from a genomic fragment of a sample of naturally occurring bacteria.
108. The method of claim 107, wherein said naturally occurring bacteria are marine proteobacteria.

109. The method of claim 107, wherein said naturally occurring bacteria are SAR86 bacteria.
110. The method of claim 107, wherein said naturally occurring bacterial genomic fragment is retrieved from a recombinant DNA library.
111. The method of claim 110, wherein said naturally occurring bacterial genomic fragment is retrieved from a bacterial artificial chromosome library.
112. The method of claim 107, wherein said genomic fragment is retrieved from a clone, wherein said clone is a member of the group consisting of BAC31A8, BAC40E8, BAC41B4, BAC64A5, HOT0m1, HOT75m1, HOT75m3, HOT75m4, HOT75m8, MB0m1, MB0m2, MB20m2, MB20m5, MB20m12, MB40m1, MB40m5, MB40m12, MB100m5, MB100m7, MB100m9, MB100m10, PALB1, PALB2, PALB5, PALB7, PALB6, PALB8, PALE1, PALE6 and PALE7.
113. The method of claim 106, wherein said host is an artificial membrane system.
114. The method of claim 106, wherein said host is a cell membrane obtained from a bacterium.

115. The method of claim 114, wherein said host is a cell membrane preparation obtained from a bacterium.
116. The method of claim 106, wherein said host is a cell membrane obtained from an eukaryote.
117. The method of claim 116, wherein said host is a cell membrane preparation obtained from an eukaryote.
118. The method of claim 106, further comprising the step of providing a light source for illuminating said light absorbing pigment, whereby said energy generator converts light into biochemical energy.
119. The method of claim 118, wherein said light source is a fast-pulsed light source.
120. The method of claim 119, wherein said fast-pulsed light source comprises a mechanism for delivering intermittent fast-light pulses at predetermined time intervals.
121. The method of claim 118, wherein said light source is a light source exhibiting different predetermined wavelengths.
122. The method of claim 106, further comprising the step of providing a mediator for mediating energy generated by said energy generator into chemical, mechanical or electrical energy.

123. The method of claim 106, wherein said proteorhodopsin protein is selected to determine an absorption spectra of said light absorbing pigment.
124. A PCR apparatus for amplifying a proteorhodopsin gene from DNA samples of naturally occurring microbial populations using polymerase chain reaction, comprising oligodeoxynucleotide primers with a Watson-Crick base pair complementarity to 5' and 3' ends of said proteorhodopsin gene.
125. The apparatus of claim 124, wherein said primers are according to Sequence ID No:2 and Sequence ID No:3.
126. A method of designing PCR primers, comprising the steps of:
- (a) determining a DNA sequence of a proteorhodopsin gene; and
 - (b) based on said determined DNA sequence in (a), designing oligodeoxynucleotide primers with a Watson-Crick base pair complementarity to said 5' and 3' ends of said proteorhodopsin gene.
127. The method of claim 126, further comprising the step of using said oligodeoxynucleotide primers to amplify said proteorhodopsin gene from DNA samples of naturally occurring microbial populations by polymerase chain reaction.
128. The method of claim 127, further comprising the step of cloning said amplified proteorhodopsin gene into an expression vector.

129. The method of claim 126, wherein said primers are according to Sequence ID No:2 and Sequence ID No:3.

**Fig. 1**

29

accatgggta aattattact gatattagg

Figure 2

24

agcattagaa gattctttaa cagc

Figure 3


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atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca      48
Met Gly Lys Leu Leu 5 tta ggt agt gtt att gca ctt cct aca      15
1
ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt      96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30
tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc      144
Ser Phe Trp Leu Val Thr Ala Thr Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45
ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tta act      192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60
gta tct ggt ctt gtt act ggt att gct ttc ttc tgg cat tac atg tac atg      240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80
aga ggg gta tgg att gaa act ggt gat tgc cca act gta ttt aga tac      288
Arg Gly Val Trp Ile Glu Thr Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95
att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta      336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

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Figure 4

att ctt gct gct gca act aat gtt gct gga tca tta ttt aag aaa tta	384
Ile Leu Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	
gga atc atg atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg	480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp	
145 150 155 160	
gta tac atg atg att tat gaa tta tgg gct gga gaa gga aaa tct gca tgt	528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys	
165 170 175	
aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat	576
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr	
180 185 190	
att atc atc ttt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt	624
Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly	
195 200 205	
tac ctg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat	672
Tyr Leu Met Gly Asp Gly Ser Ala Leu Asn Leu Ile Tyr	
210 215 220	

Figure 4

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Trp 240
225 230 235

aat gtt gct gtt aaa gaa tct tct aat gct 750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 4

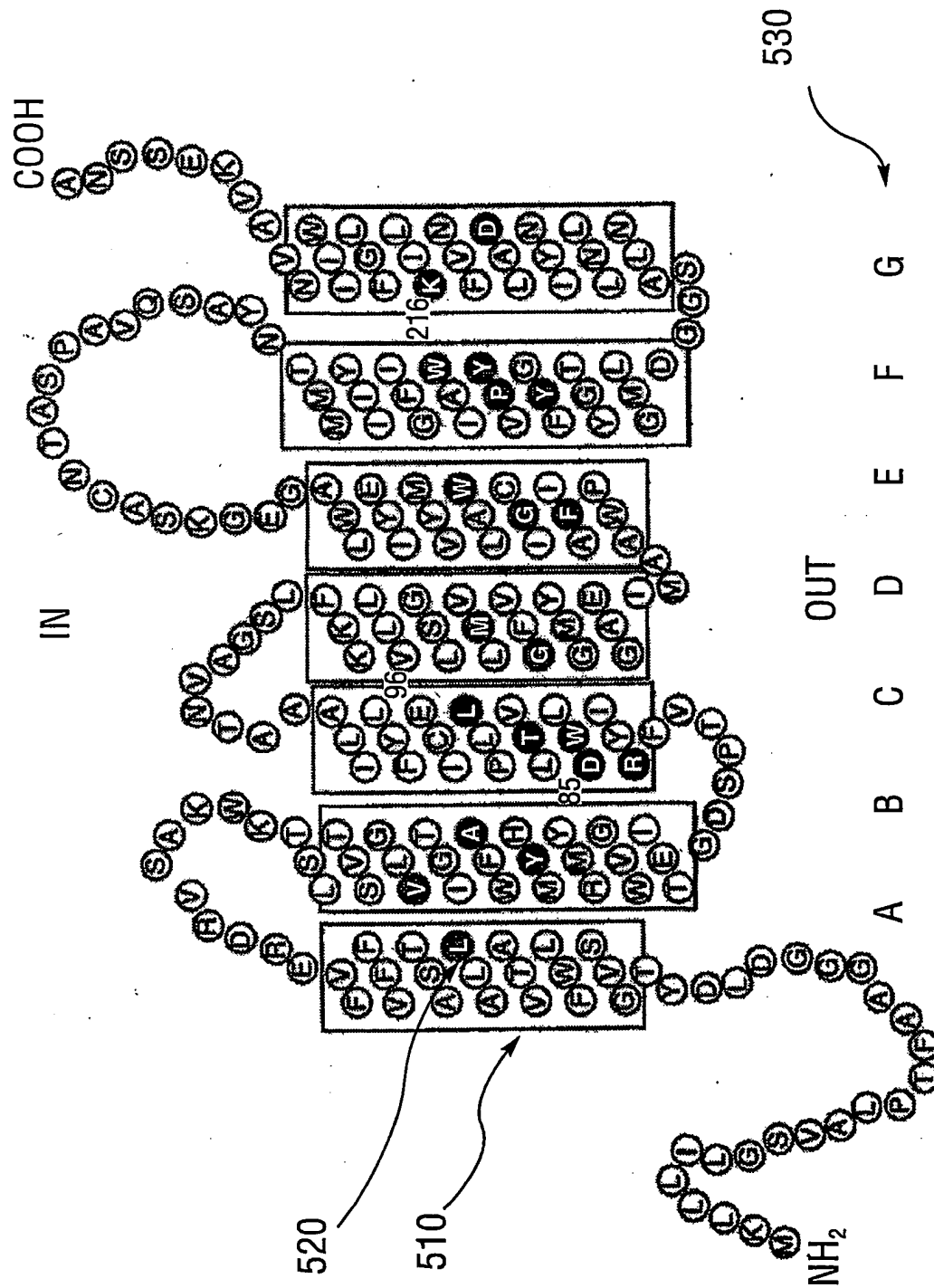


Fig. 5

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr	
1 5 10 15	
ttt gct gca ggt ggt ggt gac ctt gat gct agt gat act ggt gtt	96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val	
20 25 30	
tct ttt tgg tta gtt act gct gct cta tta gca tct act gta ttt ttc	144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe	
35 40 45	
ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tta act	192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	
gta tcg ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg	240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met	
65 70 75 80	
aga ggg gta tgg att gag act ggt gat tcg cca act gta ttt aga tac	288
Arg Gly Val Trp Ile Glu Thr Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta cta aca gtt cct cta ttg ata tgt gaa ttc tac tta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu	
100 105 110	

Figure 6

att ctt gct gct gca aca aat gtt gct gct ggc ctg ttt aag aaa tta	384
Ile Leu Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu	
115 120 125	
ttg gtt ggt tct ctt gtt atg ctt gtt ggt tac atg ggt gag gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	
gga att atg aac gct tgg ggt gca ttc gtt att ggg tgt tta gct tgg	480
Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp	
145 150 155 160	
gta tac atg att tat gaa cta tgg gct gga gaa ggc aag gct gca tgt	528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys	
165 170 175	
aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat	576
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr	
180 185 190	
ata atc atc ttt ggt tgg gca att tat cct gta ggt tat ttc aca ggt	624
Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly	
195 200 205	
tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat	672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Ile Tyr	
210 215 220	

Figure 6

gac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
Asp Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Trp 240
225 230 235

aat gtt gct gtt aaa gaa tct tct aat gct 750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 6

```

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca      48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1      5      10      15

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt      96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
      20      25      30

tct ttt tgg tta gct act gct gct tta tta gca tct act gta ttt ttc      144
Ser Phe Trp Leu Ala Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
      35      40      45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tta act      192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
      50      55      60

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg      240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
      65      70      75      80

aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac      288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
      85      90      95

att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta      336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
      100      105      110

```

Figure 7

Figure 7

Figure 7

aac ctt gct gat ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
Asn Leu Ala Asp Phe Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Trp 240
225 230 235

aat gtt gct gtt aaa gaa gaa tct tct aat gct 750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 7

```

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca      48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1      5      10      15

ttt gct gca ggt ggc ggt ggt gac ctt gat gct agt gat tac act ggt gtt      96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20      25      30

tct ttt tgg tta gtt aca gct gct gct cta tta gca tct act gta ttt ttc      144
Ser Phe Trp Leu Val Thr Ala Thr Ala Leu Ala Ser Thr Val Phe Phe
35      40      45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act      192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50      55      60

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg      240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65      70      75      80

aga gga gta tgg att gaa act ggt gat tgc cct act gta ttt aga tac      288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85      90      95

att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta      336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100      105      110

```

Figure 8

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att ctt gct gct gca act aat gtt gcc ggc tca tta ttt aag aaa ctt      384
Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120
cta gtt ggt tct ctt gtt atg ctt gtt ggt ttt ggt tac atg ggt gaa gca      432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140
gga att atg gca gct tgg cct gca ttc att att ggg tgt tta gct tgg      480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160
gta tac atg att tat gaa cta tat gct gga gaa gga aaa tct gca tgt      528
Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
165 170
aat act gca agt cct tcg gtt caa tca gct tac aac aca atg atg gct      576
Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala
180 185 190
atc ata gtc ttc ggt tgg gca att tat cct ata ggt tat ttc aca ggt      624
Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Ile Ile Gly Tyr Phe Thr Gly
195 200 205
tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt att tat      672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Ile Tyr
210 215 220

```

Figure 8

aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggt	tta	att	ata	tgg	720
Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp	
225					230					235					240	
aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct							750
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala							
				245					250							

Figure 8

EBAC31A8	1	atgggtaaat	tattactgat	attaggTAGT	GTTATTGCAC	TTCC	TACATT	50
EBAC40	1	50
EBAC41	1	50
EBAC64	1	50
EBAC31A8	51	TGCTGCAGGT	GGTGGTGACC	TTGATGCTAG	TGATTACACT	GGTGTTTCTT		100
EBAC40	51	100
EBAC41	51	100
EBAC64	51	C.....	100
EBAC31A8	101	TTTGGTTAGT	TACTGCTGCT	TTATTAGCAT	CTACTGTATT	TTTCTTTGTT		150
EBAC40	101	C.....	150
EBAC41	101	C.....	150
EBAC64	101	A.....	C.....	150
EBAC31A8	151	GAAAGAGATA	GAGTTTCTGC	AAAATGGAAA	ACATCATTAA	CTGTATCTGG		200
EBAC40	151	G..	200
EBAC41	151	200
EBAC64	151	200
EBAC31A8	201	TC TTGT TACT	GGTATTGCTT	TCTGGCATT	CATGTACATG	AGAGGGGTAT		250
EBAC40	201	250
EBAC41	201	250
EBAC64	201	A....	250
EBAC31A8	251	GGATTGAAAC	TGGTGATTG	CCAACGTGAT	TTAGATACAT	TGATTGGTTA		300
EBAC40	251	G.....	300
EBAC41	251	300
EBAC64	251	T.....	300

Figure 9

EBAC31A8	301	CTAACAGTTC	CTCTATTAAAT	ATGTGAATTC	TACTTAATTC	TTGCTGCTGC	350
EBAC40	301G.	350
EBAC41	301	350
EBAC64	301T.	350
EBAC31A8	351	AACTAATGTT	GCTGGATCAT	TATTTAAGAA	ATTACTAGTT	GGTTCTCTTG	400
EBAC40	351	...A.....	...CTGGCC	...G.....	...T.G...	400
EBAC41	351	T.....	400
EBAC64	351C.C....C.T.	400
EBAC31A8	401	TTATGCTTGT	GTTTGGTTAC	ATGGGTGAAG	CAGGAATCAT	GGCTGCATGG	450
EBAC40	401G.T..	...AAC..T...	450
EBAC41	401	450
EBAC64	401T..	...A..T...	450
EBAC31A8	451	CCTGCATTCA	TTATTGGGTG	TTTAGCTTGG	GTATACATGA	TTTATGAATT	500
EBAC40	451	GG.....GC.	500
EBAC41	451C.	500
EBAC64	451C.	500
EBAC31A8	501	ATGGGCTGGA	GAAGGAAAAT	CTGCATGTAA	TACTGCAAGT	CCTGCTGTGC	550
EBAC40	501C..GG	550
EBAC41	501	550
EBAC64	501	..AT.....T.G..T.	550
EBAC31A8	551	AATCAGCTTA	CAACACAATG	ATGTATATTA	TCATCTTTGG	TTGGGCGATT	600
EBAC40	551A.A..	600
EBAC41	551	600
EBAC64	551GC...C.	..AG....C..A...	600

Figure 9

EBAC31A8	601	TATCCTGTAG	GTTATTTCAC	AGGTTACCTG	ATGGGTGACG	GTGGATCAGC	650
EBAC40	601A	650
EBAC41	601	650
EBAC64	601AA	650
EBAC31A8	651	TCTTAACTTA	AACCTTATCT	ATAACCTTGC	TGACTTTGTT	AACAAGATTC	700
EBAC40	651G	700
EBAC41	651T	700
EBAC64	651T	700
EBAC31A8	701	TATTTGTTT	AATTATATGG	AATGTTgctg	ttaaagaatc	ttctaagtct	750
EBAC40	701	750
EBAC41	701	750
EBAC64	701	750

Figure 9

EBAC31A8	1	MGKLLILIGS	VIALPTFAAG	GGDLASDYT	GVSEWLVTA	LLASTVFEFV	50
EBAC40_1	1	50
EBAC41_1	1A.....	50
EBAC64_1	1	50
EBAC31A8	51	ERDRVSAKWK	TSLTVSGLVT	GIAFWHYMYM	RGVWIEGTGS	PTVFRYIDWL	100
EBAC40_1	51	100
EBAC41_1	51	100
EBAC64_1	51	100
EBAC31A8	101	LTVPLLICEF	YLILAAATNV	AGSLFKKLLV	GSLVMLVFGY	MGEAGIMAAW	150
EBAC40_1	101AG.....N.....	150
EBAC41_1	101	150
EBAC64_1	101	150
EBAC31A8	151	PAFIIGCLAW	VYMIYELWAG	EGKSACNTAS	PAVQSAYNMTM	MYIIIFGWAI	200
EBAC40_1	151	G..V.....A.....	200
EBAC41_1	151	200
EBAC64_1	151Y.....	S.....	A..V.....	200
EBAC31A8	201	YPVGYFTGYL	MGDGGGSA	NLNLADEFV	NKILFGLIIW	NVAVKESSNA	250
EBAC40_1	201D.....	250
EBAC41_1	201	250
EBAC64_1	201	I.....	250

Figure 10

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca
 Met Gly Lys Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15 48

 ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30 96

 tct ttt tgg tta gtt act gct gct gct cta tta gca tct act gta ttt ttc
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45 144

 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tta act
 Phe Val Glu Arg Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60 192

 gta tcg ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80 240

 aga ggg gta tgg att gag acc ggt gat tcg cca act gta ttt aga tac
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95 288

 att gat tgg tta cta aca gtt cct cta ttg ata tgt gaa ttc tac tta
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110 336

Figure 11

att ctt gct gct gca aca aat gtt gct gct ggc ctg ttt aag aaa tta 384
 Ile Leu Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
 115 120 125
 ttg gtt ggt tct ctt gtt atg ctt gtt ggt tac atg ggt gag gca 432
 Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140
 gga att atg aac gct tgg ggt gca ttc gtt att ggg tgt tta gct tgg 480
 Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp
 145 150 155 160
 gta tac atg att tat gaa cta tgg gct gga gaa ggc aag gct gca tgt 528
 Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys
 165 170 175
 aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat 576
 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190
 ata atc atc ttt ggt tgg gca att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205
 tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Ile Tyr
 210 215 220

Figure 11

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp 240
225 230 235

aat gtt gct gtt aaa gaa tct tct aat gct 750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245 250

Figure 11

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15
 ttt gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30
 tca ttc tgg ctg ctg gtt aca gct gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
 35 40 45
 ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt gct 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Ala
 50 55 60
 gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80
 aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Figure 12

att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125

cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140

gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg 480
 Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta 528
 Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175

agt act gca agt cct gct gct gtt aac tct gca tac aac gca atg atg atg 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
 180 185 190

att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

tac cta atg ggt ggc gaa ggt gta tac gct tca aac tta aac ctt ata 672
 Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Figure 12

tat aac ctt gcc gac ctt gtt aac aag att cta ttt ggt ttg atc att 720
Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile 240
225 230 235

tgg aat gtt gct gtt aaa gaa tct tct aat gct 753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 12

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atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca      48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1      5      10      15

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt      96
Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20      25      30

tca ttc tgg ctg ctg gtt aca gct ggt atg tta gcg gca act gta ttc ttt      144
Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
35      40      45

ttt gta gaa aga gac caa gtc agc gct agt aag tgg aaa act tca ctt act      192
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50      55      60

gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tac atg      240
Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65      70      75      80

aga ggt gtt tgg ata gat act ggt gat aca cca aca gta ttt aga tat      288
Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85      90      95

att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta      336
Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100      105      110

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Figure 13

att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125
 cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140
 ggt tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg 480
 Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160
 tta tac atg att tat gag cta cat atg ggt gaa ggt aag gct gct gta 528
 Leu Tyr Met Ile Tyr Glu Leu His Met Gly Glu Tyr Lys Ala Ala Val
 165 170 175
 agt act gca agt cct gct gct gtt aac tct gca tac aac gca atg atg aag 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Lys
 180 185 190
 att att gtt att gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205
 tac cta atg agt ggt gac ggt gta tac gct tca aac tta aac ctt ata 672
 Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Figure 13

tat aac ctt gct gac gtt gtt aac aag att cta ttt ggt ttg atc att	720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile	240
225	230
235	
240	
245	
250	
255	
260	
265	
270	
275	
280	
285	
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970	
975	
980	
985	
990	
995	
1000	

Figure 13

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu 5
 1 10 15
 ttt gct gct ggt ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30
 tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
 35 40 45
 ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80
 aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta tta act gtt cca tta caa gtg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Val Val Glu Phe Tyr Leu
 100 105 110

Figure 14

att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt	384
Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct	432
Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala	
130 135 140	
gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg	480
Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp	
145 150 155 160	
tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta	528
Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val	
165 170 175	
agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg	576
Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met	
180 185 190	
att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt	624
Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly	
195 200 205	
tac cta atg ggt ggc gaa ggt gta tac gct tca aac tta aac ctt ata	672
Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile	
210 215 220	

Figure 14

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att	720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile	240
225	230
tgg aat gtt gct gtt gaa gaa tct tct aat gct	753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala	250
245	240

Figure 14

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15
 ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30
 tca ttc tgg ctg gtt gtt aca gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
 35 40 45
 ttt gta gaa aga gac caa gtc agc gct aag gct aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80
 aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Figure 15

att ctt gct gct tgt aca aat gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125
 cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140
 gga ttg gct cct gta tgg cct gct ttc att att ggt atg gct gga tgg 480
 Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155
 tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta 528
 Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175
 agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg gtg 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Val
 180 185 190
 att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205
 tac cta atg ggt ggc gaa ggt gta tac gct gct tca aac tta aac ctt ata 672
 Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Figure 15

tat aac ctt gcc gac gtt gtt aac aag att cta ttt ggt ttg atc att 720
Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile 240
225 230 235

tgg aat gtt gct gtt gaa gaa tct tct aat gct 753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 15

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu 5
 1
 ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30
 tct ttt tgg tta gtt act gct gct gct cta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45
 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80
 aga ggg gta tgg att gag act ggt gat ggt gat tgg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta cta aca gtt cct cta tta gaa gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Figure 16

att ctt gct gct gca aca aat gtt gct gct ggc ctg ttt aag aaa tta 384
 Ile Leu Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
 115 120 125
 ttg gtt ggt tct ctt gtt atg ctt gtt ggt tac atg ggt gag gca 432
 Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140
 gga att atg aac gct tgg cct gca ttc att att ggg tgt tta gct tgg 480
 Gly Ile Met Asn Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
 145 150 155 160
 gta tac atg att tat gaa cta tat gct gga gaa gga aaa tct gca tgt 528
 Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Tyr Lys Ser Ala Cys
 165 170 175
 aat act gca agt cct tcg gtt caa tca gct tac aac aca atg atg gct 576
 Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala
 180 185 190
 atc ata gtc ttc ggt tgg gca att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205
 tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt att tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Ile Tyr
 210 215 220

Figure 16

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Trp 240
225 230

aat gtt gct gtt aaa gaa tct tct aat gct 750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 16

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atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca      48
Met Gly Lys Leu Leu 5 tta ctg ata tta ggt agt gtt att gca ctt cct aca
1                               10
                               15
ttt gct gca ggt ggt ggt gac ctt gat gct agt gat gtt ggt ggt gtt      96
Phe Ala Ala Gly Gly Gly ggt ggt ggt gct gct agt gat gtt ggt ggt ggt
20                               25
30
tct ttt tgg tta gtt act gct gct gct tta tta gca tct act gta ttt ttc      144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35                               40
45
ttt gtt gaa aga gat aga gtt tct tct gca aaa tgg aaa aca tta act      192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50                               55
60
gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg      240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65                               70
75
80
aga ggg gta tgg att gaa act ggt gat tgg cca act gta ttt aga tac      288
Arg Gly Val Trp Ile Glu Thr Thr Gly Asp Ser Pro Thr Phe Arg Tyr
85                               90
95
att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta      336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100                               105
110

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Figure 17

Figure 17

Figure 17

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Trp 240
225 230

aat gtt gct gtt aaa gaa tct tct aat gct 750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 17

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Ile Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15
 ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30
 tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45
 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80
 aga ggg gta tgg att gaa act ggt gat tgg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Figure 18

att ctt gct gct gca act aat gtt gct gct ggc ctg ttt aag aaa tta	384
Ile Leu Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu	
115 120 125	
ttg gtt ggt tct ctt atg gtt gtt ggt tac atg ggt gag gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	
gga att atg aac gct tgg ggt gca ttc gtt att ggg tgt tta gct tgg	480
Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp	
145 150 155 160	
gta tac atg att tat gaa cta tgg gct gga gaa ggc aag gct gca tgt	528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Lys Ala Ala Cys	
165 170 175	
aat act gca agt cct gct gct gct tca caa gct aac aca atg atg tat	576
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr	
180 185 190	
ata atc atc ttt ggt tgg gca att tat cct gta ggt tat ttc aca ggt	624
Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly	
195 200 205	
tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat	672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Ile Tyr	
210 215 220	

Figure 18

aac	ctt	gct	gac	ttt	ggt	aac	aag	att	cta	ttt	ggt	tta	att	ata	tgg	720
Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp	
225				230						235					240	
aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct							750
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala							
				245					250							

Figure 18

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu 5
 1
 ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30
 tct ttt tgg tta gtt aca gct gct cta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45
 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt ctt gtt act act ggt att gct ttc tgg cat tac atg tac atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met 80
 65 70 75
 aga ggg gta tgg att gaa act ggt gat tgg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 95
 85 90
 att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Figure 19

Figure 19

aac ctt gct gac ttt gtt aac aag att cta ctt ggt tta att ata tgg 720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Leu Gly Leu Ile Ile Trp 240
225 230

aat gtt gct gtt aaa gaa tct tct aat gct 750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 19

48
 atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15
 96
 ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30
 144
 tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45
 192
 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tta act
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 240
 gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80
 288
 aga ggg gta tgg att gaa act ggt gat tgg cca act gta ttt aga tac
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95
 336
 att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Figure 20

att ctt gct gct gca gct aat gtt gct gga tca tta ttt aag aaa tta	384
Ile Leu Ala Ala Ala Val Asn Val Ala Gly Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	
gga atc atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg	480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp	
145 150 155 160	
gta tac atg att tat gaa tta tgg gct gga gaa gga aaa tct gca tgt	528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys	
165 170 175	
aat act gca agt cct gct gct gtg caa tca gcc tac aac aca atg atg tat	576
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr	
180 185 190	
att atc atc ttt ggt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt	624
Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly	
195 200 205	
tac ttg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat	672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Ile Tyr	
210 215 220	

Figure 20

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Trp 240
225 230 235

aat gtt gct gtt aaa gaa tct tct aat gct 750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245 250

Figure 20

atg ggt aaa tta tta ctg ata ata ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu 5
 1
 ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30
 tct ttt tgg tta gtt aca gct gct gct cta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Thr Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45
 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt ctt gtt act act ggt att gct ttc tgg cat tac atg tac atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80
 aga gga gta tgg att gaa act ggt gat gct gat tcg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Figure 21

att ctt gct gct gca act aat gtt gcc ggc tca tta ttt aag aaa ctt 384
 Ile Leu Ala Ala 115 Val Asn Val Ala Gly Ser Leu Phe 125 Lys Lys Leu
 cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca 432
 Leu Val Gly Ser Leu Val Met Leu Val Phe Phe Gly Tyr Met Gly Glu Ala
 130 135 140
 gga att atg gca gct tgg cct gca ttc att att ggg tgt tta gct tgg 480
 Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
 145 150 155 160
 gta tat atg att tat gaa cta tat gct gga gaa gga aaa tct gca tgt 528
 Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175
 aat aca gca agt cct gct gtg caa tca gct tac aac aca atg atg tat 576
 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190
 att atc gtc ttt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205
 tac ctg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Ile Tyr
 210 215 220

Figure 21

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Trp 240
225 230 235

aat gtt gct gtt aaa gaa tct tct aat gct 750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 21

atg ggt aaa tta tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15
 ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30
 tct ttt tgg tta gtt act gct gct gct cta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45
 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tcg ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80
 aga ggg gta tgg att gag act gag act ggt gat tcg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta cta aca gtt cct cta ttg ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Figure 22

att ctt gct gct gca aca aat gtt gct gct ggc ctg ttt aag aaa tta 384
 Ile Leu Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
 115 120 125
 ttg gtt ggt tct ctt gtt atg ctt gtt ttt ggt tac atg ggt gag gca 432
 Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140
 gga att atg aac gct tgg ggt gca ttc gtt att ggg tgt tta gct tgg 480
 Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp
 145 150 155 160
 gta tac atg att tat gaa cta tgg gct gga gaa ggc aag gct gca tgt 528
 Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys
 165 170 175
 aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat 576
 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190
 ata atc atc ttt ggt gca att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205
 tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Ile Tyr
 210 215 220

Figure 22

aac ctt gct gac ttt gtt aac aag aat cta ttt ggt tta att ata tgg 720
Asn Leu Ala Asp Phe Val Asn Lys Asn Leu Phe Gly Leu Ile Ile Trp 240
225 230 235

aat gtt gct gtt aaa gaa tct tct aat gct 750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245 250

Figure 22

atg ggt aaa tta tta tta cgg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Leu Arg Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15
 ttt gct gca ggt ggc ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30
 tct ttt tgg tta gtt aca gct gct gct cta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45
 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tat atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80
 aga gga gta tgg att gaa act ggt gat tgg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Figure 23

att ctt gct gct gca gct gtt gct gga tca tta ttt aag aaa tta 384
 Ile Leu 115 Ala Ala Ala Thr Asn Val 120 Phe Lys Lys Leu 125

 cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca 432
 Leu Val 130 Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 140

 gga atc atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg 480
 Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp 155
 145 150

 gta tac atg att tat gaa cta tgg gct gga gaa gga aaa tct gca tgt 528
 Val Tyr Met Ile Tyr 165 Glu Trp Ala Gly Glu Gly Lys Ser Ala Cys 170
 165

 aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat 576
 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr 180
 185

 atc atc atc gtt ggt gct tgg gcg att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Ile Val Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly 190
 195 200

 tac ctg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Ile Tyr 210
 215 220

Figure 23

720
aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp 240
225 230
aat gtt gct gtt gaa tct tct aat gct
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 23


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atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca      48
Met Gly Lys Leu Leu 5 tta ggt agt gtt att gca ctt cct aca      15
1
ttt gct gca ggt ggc ggt ggt gac ctt gat gct agt gat tac act ggt gtt      96
Phe Ala Ala Gly Gly Gly Thr Ala Thr Ala Ala Leu Leu Ala Ser Asp Tyr Thr Gly Val
20 25 30
tct ttt tgg tta gtt aca gct gct gct cta tta gca tct act gta ttt ttc      144
Ser Phe Trp Leu Val Thr Ala Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45
ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act      192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60
gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg      240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80
aga gga gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac      288
Arg Gly Val Trp Ile Glu Thr Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95
att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta      336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

```

Figure 24

att ctt gct gct gca act aat gtt gcc gcc tca tta ttt aag aaa ctt 384
 Ile Leu Ala Ala gct gca act Thr Asn Val Ala Gly Ser Leu Phe Lys Leu
 115 120 125

 cta gtt ggt tct ctt gtt atg ctt gtt ggt tac atg ggt gaa gca 432
 Leu Val Gly Ser Leu Leu Val Met Leu Phe Gly Tyr Met Gly Glu Ala
 130 135 140

 gga att atg gca gct tgg cct gca ttc att att ggg tgt tta gct tgg 480
 Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
 145 150 155 160

 gta tac atg att tat gaa cta tat gct gga gaa gga aaa tct gca tgt 528
 Val Tyr Met Ile Tyr Ala Tyr Ala Gly Glu Glu Gly Lys Ser Ala Cys
 165 170 175

 aat act gca agt cct tcg gtt caa tca gct tac aac aca atg atg gct 576
 Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala
 180 185 190

 atc ata gtc ttc ggt tgg gca att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

 tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt att tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Ile Tyr
 210 215 220

Figure 24

720
aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp 240
225
230
235
750
aat gtt gct gtt aaa gaa tct tct aat gct
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 24

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15
 ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30
 tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45
 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80
 aga ggg gta tgg att gaa act ggt gat tgg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Figure 25

Figure 25

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
Asn Leu Ala Asp Phe Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Trp 240
225 230 235

aat gct gct gtt gtt aaa gaa tct tct aat gct 750
Asn Ala Ala Val Lys Lys Glu Ser Ser Asn Ala 250
245

Figure 25

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu 5
 1
 ttt gct gca ggt ggt ggt gac gct gct gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30
 tct ttt tgg tta gtt act gct gct gct tta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45
 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tat atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80
 aga ggg gta tgg att gaa act ggt gat tgg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95
 ata gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Figure 26

att ctt gcc gct gct gca act aat gtt gct gga tca tta ttt aag aaa tta 384
 Ile Leu Ala Ala gct gct gtt gtt gca ttc att gga gaa ggt ggt gaa gca
 115 120 125
 ctt gtt ggt tct ctt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt 432
 Leu Val Gly Ser Ile ctt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt
 130 135 140
 gga atc atg gct gct gca tgg cct gca ttc att ggt tta gct tgg 480
 Gly Ile Met Ala Ala gct gct gca ttc att ggt tta gct tgg
 145 150 155 160
 gta tac atg att tat gaa cta tgg gct gga gaa gga gaa tct gca tgt 528
 Val Tyr Met Ile Tyr Ala Trp Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175
 aat act gca agt cct gct gct gct gct gct gct gct gct gct gct gct gct 576
 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190
 atc atc atc ttt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt 624
 Ile Ile Ile Phe Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205
 tac ctt atg ggt gac ggt gga tca gca ctt aac tta aac ctt att tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Ile Tyr
 210 215 220

Figure 26

720
aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Trp 240
225 230 235
aat gtt gct gtt gaa tct tct aat gct
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 26

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15
 ttt gct gca ggt ggc ggt gac ctt gat gct agt gat act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30
 tct ttt tgg tta gtt aca gct gct gct cta tta gcg tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45
 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tat atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80
 aga gga gta tgg att gaa act ggt gat tgg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Figure 27

att ctt gct gct gca act aat gtt gcc ggc tca tta ttt aag aaa ctt 384
 Ile Leu Ala Ala gct gca act Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
 115 120 125

 cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca 432
 Leu Val Gly Ser Leu Val Met Leu Val Phe Phe Gly Tyr Met Gly Glu Ala
 130 135 140

 gga ata atg gcg gct tgg cct gca ttc atc gtt gga tgt tta gca tgg 480
 Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Val Gly Cys Leu Ala Trp
 145 150 155 160

 gta tat atg att tat gaa cta tgg gct ggt gaa gga aaa tct gca tgt 528
 Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175

 aat act gca agt cct gct gta cag tca gct tac aac aca atg atg tat 576
 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

 atc atc atc gtt ggt gca att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Ile Val Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

 tac cta atg ggt gac ggt gga tca gct ctt aat cta aac ctt att tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Ile Tyr
 210 215 220

Figure 27

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Trp 240
225 230 235

aat gtt gct gtt aaa gaa tct tct aat gct 750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 27

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15
 ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Asp Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30
 tca ttc tgg ctg gtt aca gct gct ggt atg tta gcg gca act gta ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
 35 40 45
 ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tac atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80
 aga ggt gtt tgg ata gat act ggt gat aca cca gta ttt aga tat 288
 Arg Gly Val Trp Ile Asp Thr Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg cta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Figure 28

att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125
 cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140
 ggt tta gct cct gta tta cct gct ttc att ctt ggt atg gct ggt tgg 480
 Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Leu Gly Met Ala Gly Trp
 145 150 155 160
 tta tac atg att tat gag cta cat atg ggt gaa ggt aag gct gct gta 528
 Leu Tyr Met Ile Tyr Glu Leu His Met Gly Glu Lys Ala Ala Val
 165 170 175
 agt act gca agt cct gct gtt aac tct gct tac aat gca atg atg aag 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Lys
 180 185 190
 att att gtt att gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205
 tac cta atg agt ggt gac ggt gta tac gct tca aac tta aac ctt ata 672
 Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Figure 28

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att 720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile 240
225 230 235

tgg aat gtt gct gtt gaa tct tct aat gct 753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 28

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15
 ttt gct gct ggt ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30
 tca ttc tgg ctg gtt aca gct ggt ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
 35 40 45
 ttt gta gaa aga gac caa gtc agc gct gag tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Glu Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80
 aga ggt gtt tgg ata gat act ggt gat acc cca aca gta ttc aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Figure 29

att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt	384
Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct	432
Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala	
130 135 140	
gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg	480
Gly Leu Ala Pro Val Leu Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp	
145 150 155 160	
tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta	528
Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val	
165 170 175	
agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg	576
Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met	
180 185 190	
att att gtt gtt gga tgg gca att tat cct gct gct tat gct gct ggt	624
Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly	
195 200 205	
tac cta atg ggt ggc gaa ggt gta tac gct gct tca aac tta aac ctt ata	672
Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile	
210 215 220	

Figure 29

720
tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240
753
tgg aat gtt gct gtt gaa gaa tct tct aat gct
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

Figure 29

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15
 ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30
 tca ttc tgg ctg gtt aca gct gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
 35 40 45
 ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt tta att act ggt ata gcc ttt tgg cat tat ctc tat atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80
 aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Figure 30

att ctt gct gct tgt aca aat gtt gct gct tca tta ttt aag aag ctt	384
Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct	432
Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala	
130 135 140	
gga tta gct cct gta tgg cct gct ttc att att ggt atg gct gga tgg	480
Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp	
145 150 155 160	
tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta	528
Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Lys Ala Ala Val	
165 170 175	
agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg	576
Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met	
180 185 190	
att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt	624
Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly	
195 200 205	
tac cta atg ggt ggc gaa ggt gta tac gct gct tca aac cta aac ctt ata	672
Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile	
210 215 220	

Figure 30

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att 720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile 240
225 230 235

tgg aat gtt gct gtt aaa gaa tct tct aat gct 753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 30

atg ggt aaa tta tta ctg ata tta ggt agt gct att gcg ctt cca tca 48
 Met Gly Lys Leu Leu 5
 1
 ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Gly Asp Gly Asp Leu Met 25
 20
 tca ttc tgg ctg gtt acg gct gct ggt atg tta gcg gca act gta ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
 35 40 45
 ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tac atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80
 aga ggt gtt tgg ata gat act ggt gat aca cca aca gta ttt aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Figure 31

att ctt gcc gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu 115 120 125

 cta gct ggt tca ttg gta atg tta ggt gct gga tct gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Ser Ala Gly Glu Ala 130 135 140

 gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg 480
 Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp 145 150 155 160

 tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta 528
 Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Tyr Asn Ala Met Met 165 170 175

 agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met 180 185 190

 att att gtt ggt gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly 195 200 205

 tac cta atg ggt ggc gaa ggt gta tac gct tca aac tta aac ctc ata 672
 Tyr Leu Met Gly Gly Glu Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile 210 215 220

Figure 31

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att 720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile 240
225 230 235

tgg aat gtt gct gtt gtt aaa gaa tct tct aat gct 753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 31

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15
 ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30
 tca ttc tgg ctg gtt gtt aca gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
 35 40 45
 ttt gta gaa aga gac caa gtc agc gct agt tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80
 aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Figure 32

att ctt gct gct tgt aca aat gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125

 cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140

 gga tta gct cct gta tgg cct gct ttc att att ggt atg gct gga tgg 480
 Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

 tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta 528
 Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Tyr Asn Lys Ala Ala Val
 165 170 175

 agt act gca agt cct gct gct gtt aac tct gca tac aac gca atg atg gtg 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Val
 180 185 190

 att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

 tac cta atg ggt ggc gaa ggt gta tac gct tca aac cta aac ctt ata 672
 Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Figure 32

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att	720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile	240
225	
230	
235	
tgg aat gtt gct gtt aaa gaa tct tct aat gct	753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala	
245	
250	

Figure 32

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu 5
 1
 ttt gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30
 tca ttc tgg ctg gtt aca gct gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
 35 40 45
 ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt tta att act ggt ata gct gct ttt tgg cat tat ctc tat atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80
 aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Figure 33

att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125
 cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140
 gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg 480
 Gly Leu Ala Pro Val Leu Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160
 tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta 528
 Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175
 agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
 180 185 190
 att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205
 tac cta atg ggt ggc gaa ggt gta tac gct tca aac tta aac ctt ata 672
 Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Figure 33

tat aac ctt gct gac ctt gtt aac aag att cta ttt ggt ttg atc att 720
Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile 240
225 230 235

tgg aat gtt gct gtt gaa tct tct aat gct 753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 33

```

48      atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca
Met Gly Lys Leu Leu Leu 5      10      15
1      1

          ttt gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt
Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
          20      25      30
96

          tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt
Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
          35      40      45
144

          ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
          50      55      60
192

          gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg
Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
          65      70      75      80
240

          aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat
Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
          85      90      95
288

          att gat tgg tta tta act gtt cca tta caa gtg gtt gag ttc tat cta
Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Val Val Glu Phe Tyr Leu
          100      105      110
336

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Figure 34

att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125

cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140

gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg 480
 Gly Leu Ala Pro Val Leu Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

tta tac atg att tat gag cta tat atg ggt gaa ggc aag gct gct gta 528
 Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Tyr Lys Ala Ala Val
 165 170 175

agt act gca agt cct gct gtt aac cct gca tac aac gca atg atg atg 576
 Ser Thr Ala Ser Pro Ala Val Asn Pro Ala Tyr Asn Ala Met Met Met
 180 185 190

att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

tac cta atg ggt ggc gaa ggt gta tac gct tca aac tta aac ctt ata 672
 Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Figure 34

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att	720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile	240
225	
230	
235	
tgg aat gtt gct gtt gaa tct tct aat gct	753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala	250
245	

Figure 34

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15
 ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30
 tca ttc tgg ctg ctg gtt gtt aca gct gct ggt atg tta gcg gca act gta ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
 35 40 45
 ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt tta att act ggt ata gct gct ttt tgg cat tat ctc tac atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80
 aga ggt gtt tgg ata gat act ggt gat aca cca cca gta ttt aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Figure 35

att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125

cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140

ggt tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg 480
 Gly Leu Ala Pro Val Leu Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

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 180 185 190

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 Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

tac cta atg agt ggt gac ggt gta tac gct tca aac tta aac ctt ata 672
 Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Ile
 210 215 220

Figure 35

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att 720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile 240
225 230 235

tgg aat gtt gct gtt gaa tct tct aat gct 753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala 250
245

Figure 35

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
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 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30
 tca ttc tgg ctg ctg gtt aca gct gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Thr Val Phe Phe
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 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
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 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
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 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Figure 36

att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Ser Val Ala Ser Leu Phe Lys Lys Leu
 115 120 125

 cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140

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 Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

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 Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175

 agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
 180 185 190

 att att gtt ggt gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

 tac cta atg ggt ggc gaa ggc gta tac gct tca aac tta aac ctt ata 672
 Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Figure 36

tat aac ctt gct gac ttt gtt aac aag att cta	ttt ggt ttg atc att	720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu	Phe Ile Ile	240
225	230	235
tgg aat gtt gct gtt gaa tct tct aat gct		753
Trp Asn Val Ala Val Lys Glu Ser Ser-Asn Ala		250
245		

Figure 36

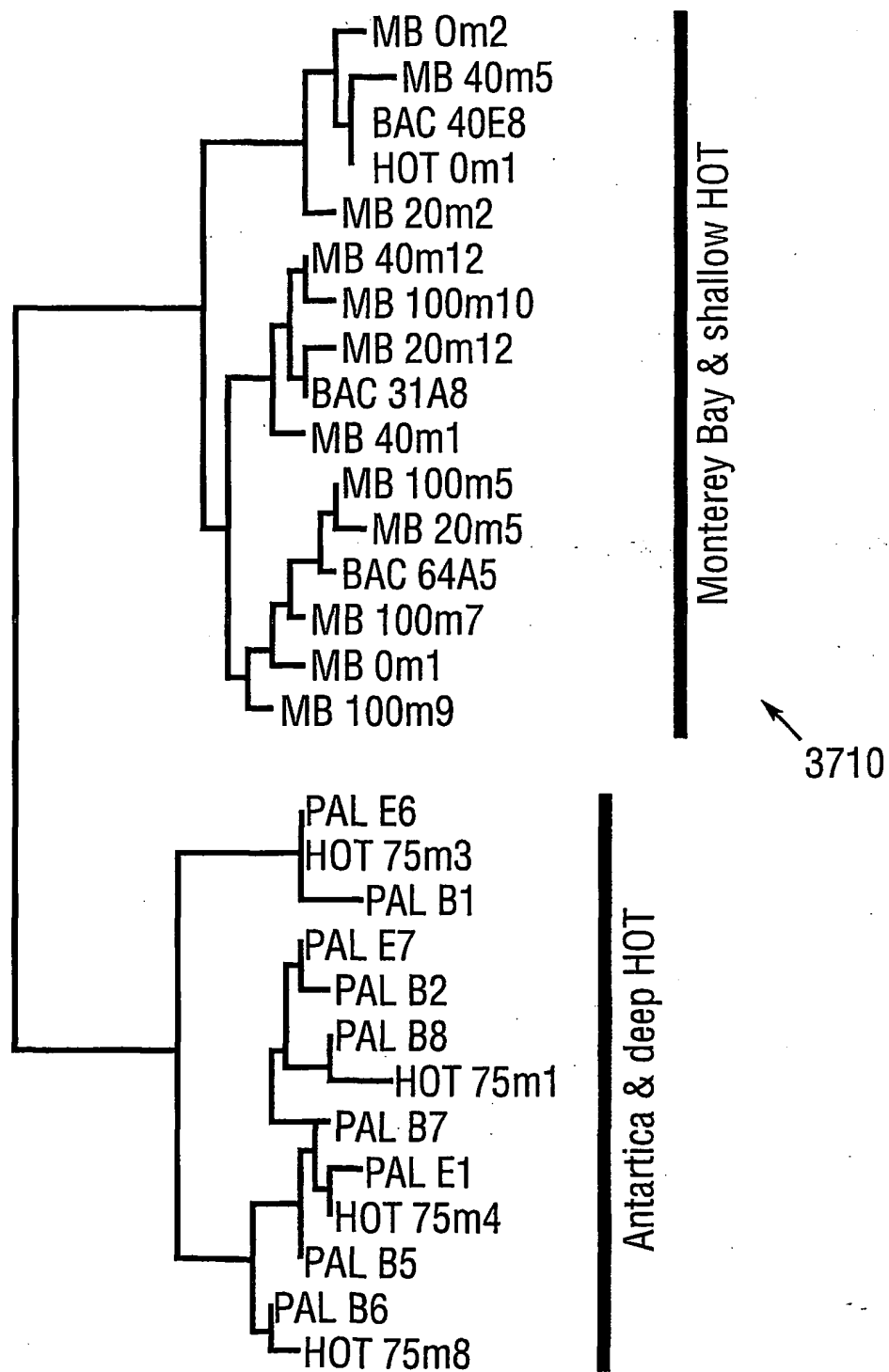
**Fig. 37**

Fig. 38A

Fig. 38A

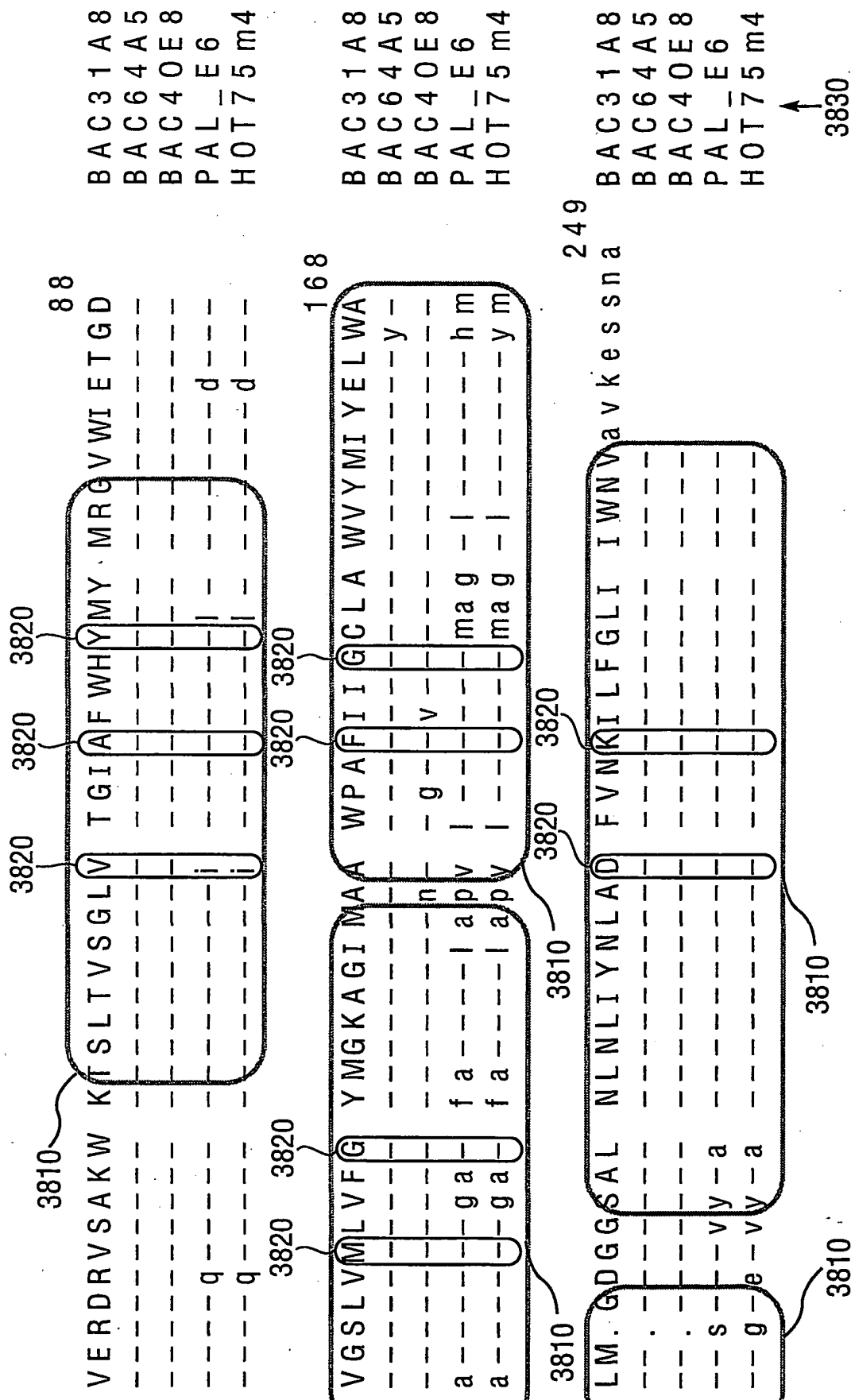


Fig. 38B

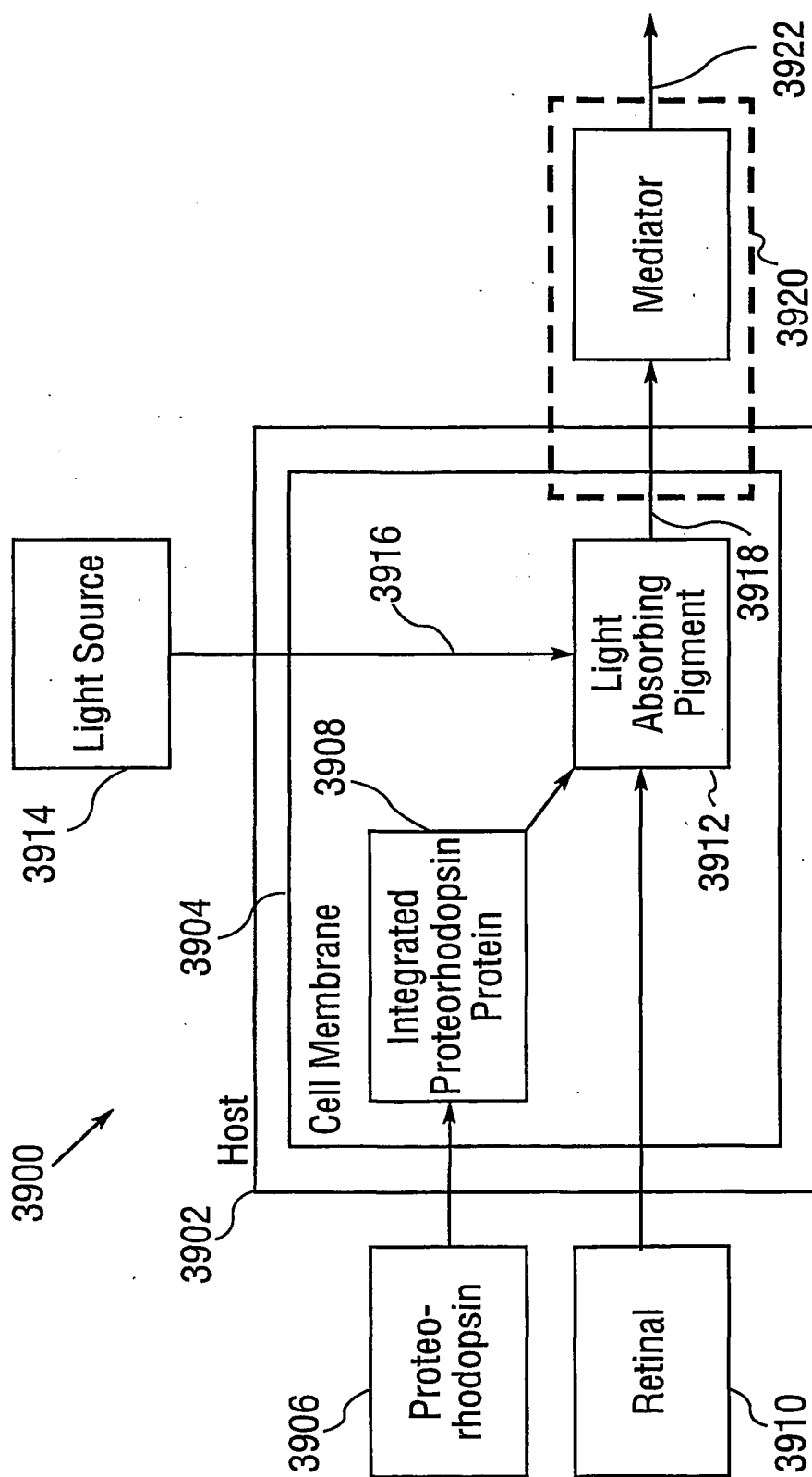
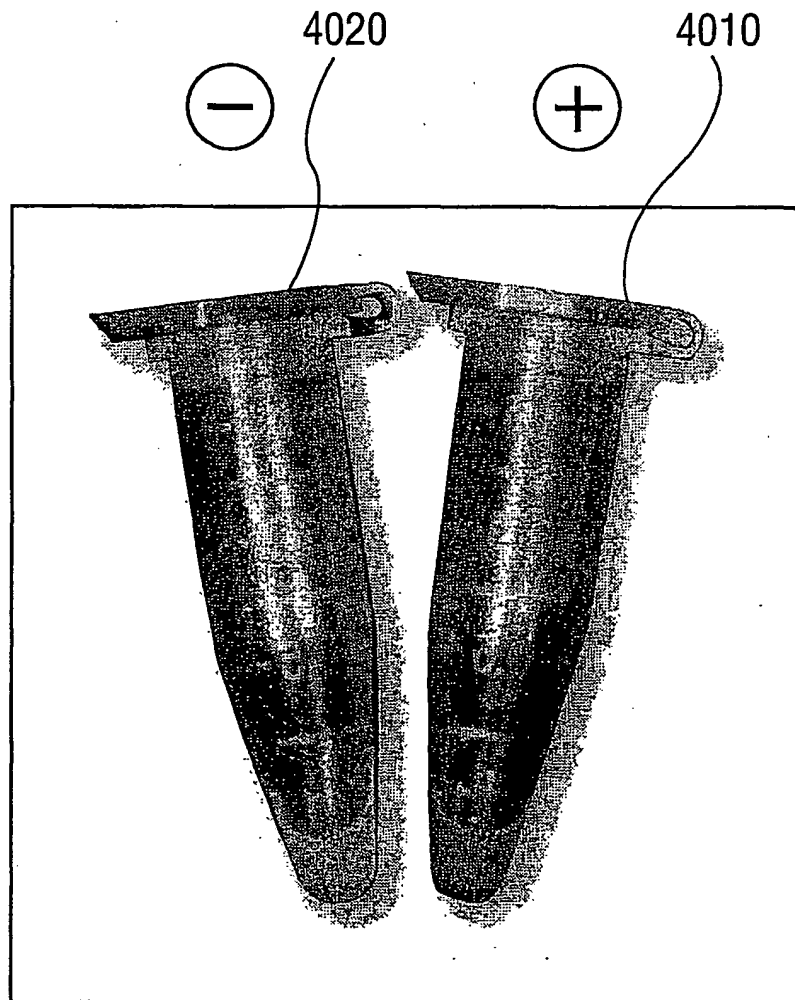


Fig. 39



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Fig. 40

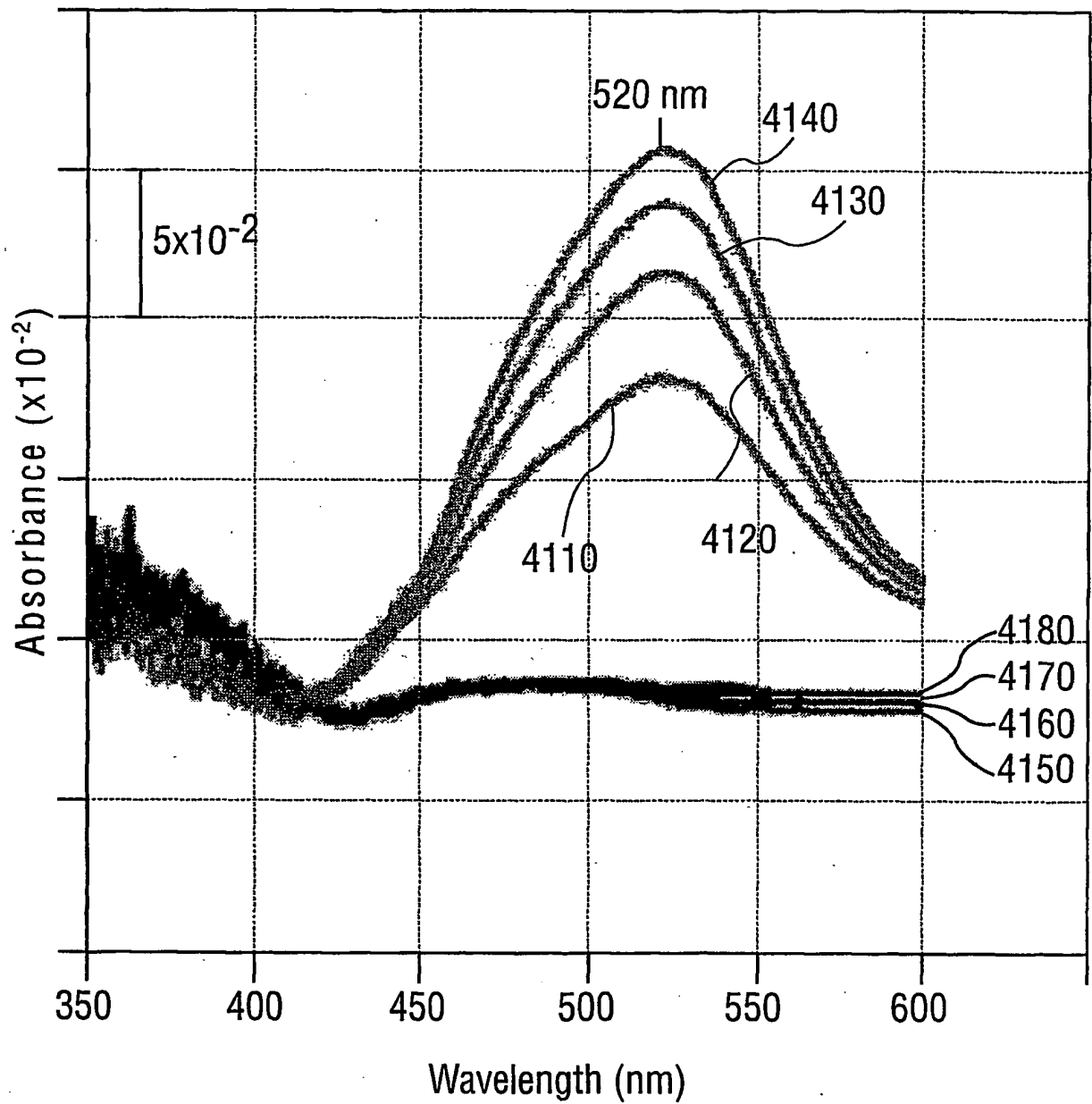


Fig. 41

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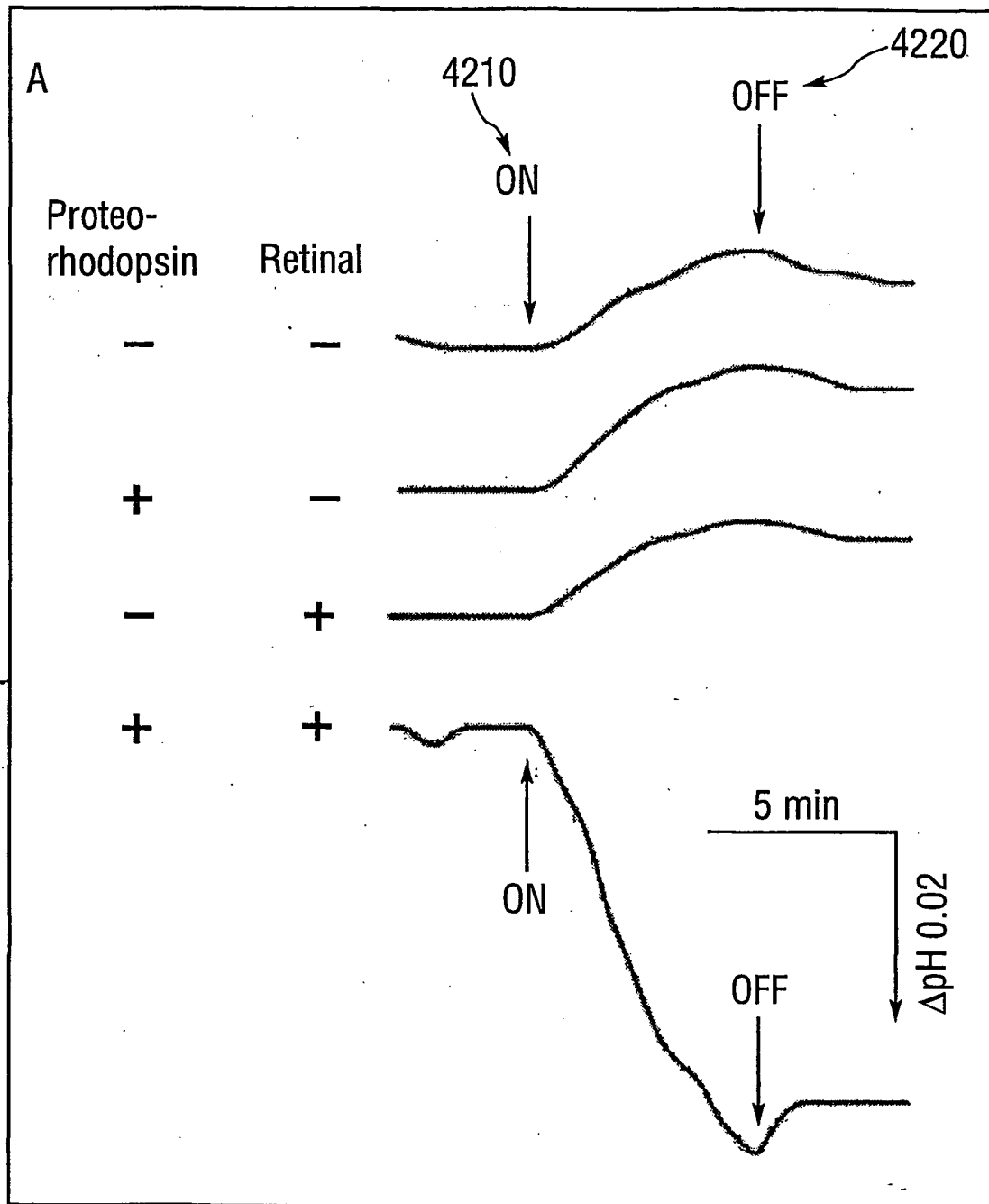


Fig. 42

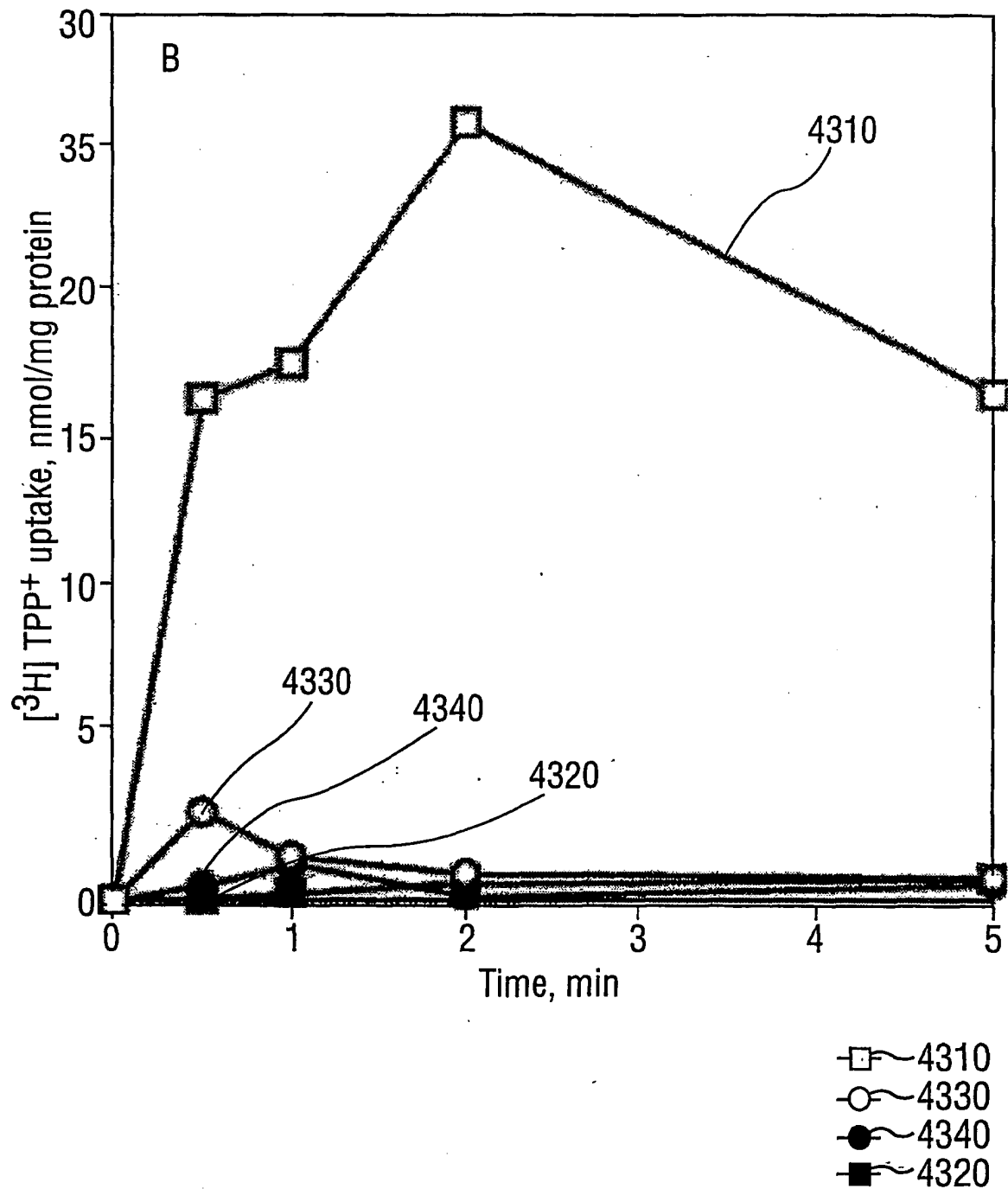
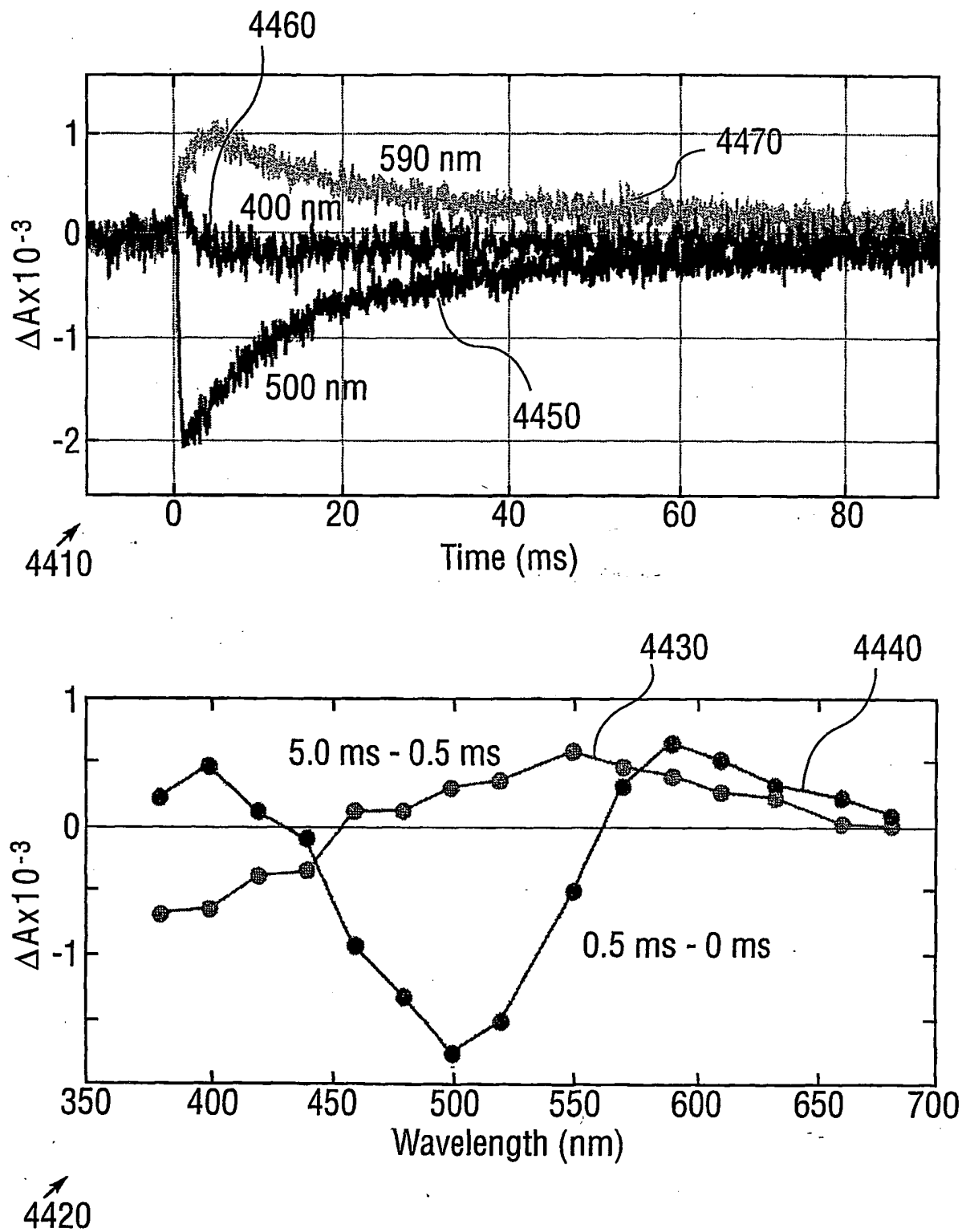
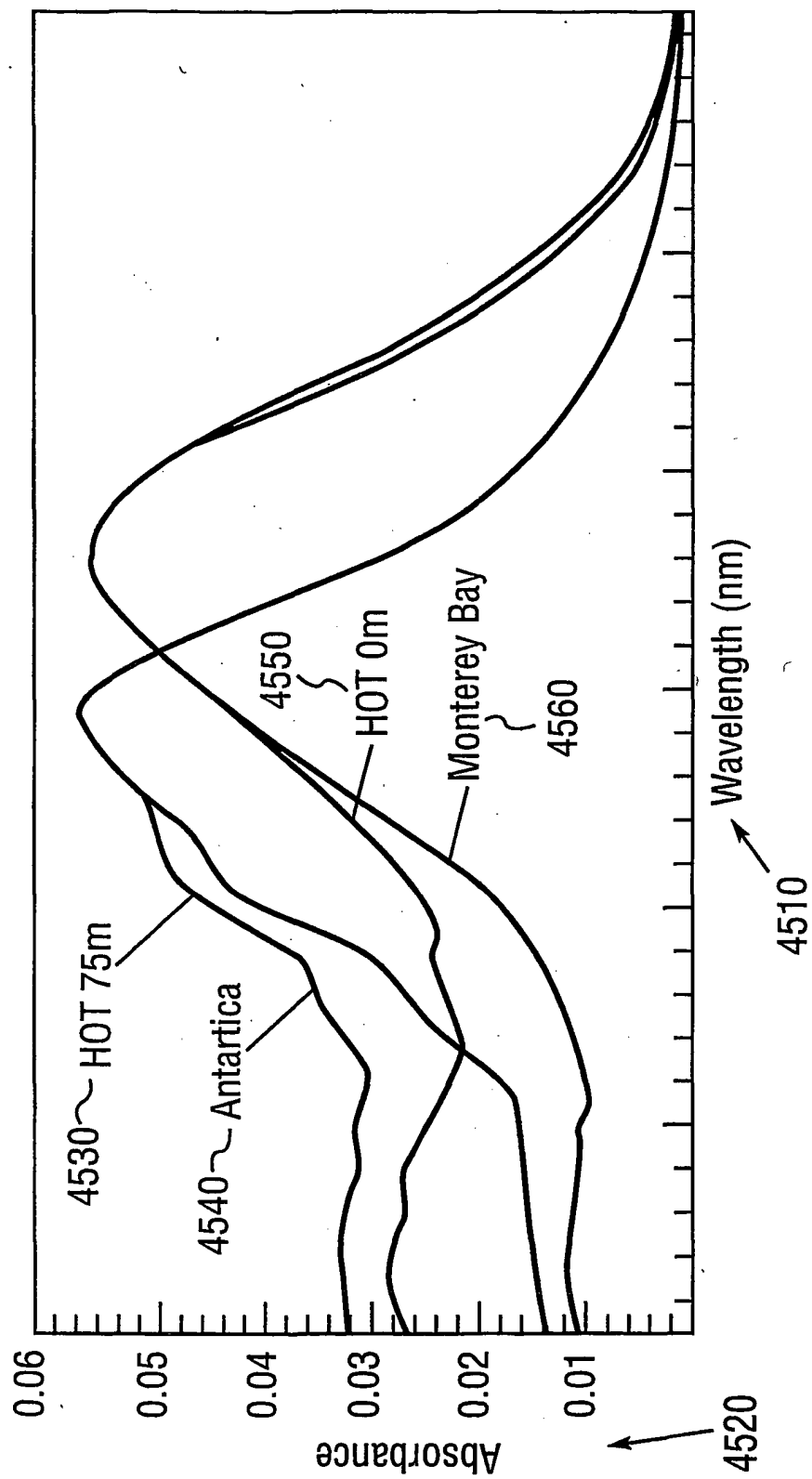


Fig. 43 BEST AVAILABLE COPY

**Fig. 44** BEST AVAILABLE COPY

**Fig. 45**

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DeLong, Edward
Beja, Oded

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<301> Beja,O., Aravind,L., Koonin,E.V., Suzuki,M.T.,
Hadd,A.,Nguyen,L.P., Jovanovich,S.B., Gates,C.M., Feldman,R.A.,
DeLong,E.F
<302> Bacterial rhodopsin: evidence for a new type of phototrophy in the sea
<303> Science
<304> 289
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taaatatgct gatacttctt ctgaagattc aaccgaaact gttccaacaa gaatgggaga 104700
agattttttt cttaattggt caatttcttc aattagagct ttatatttcg attctgttgt 104760

aagaaatact aagtcattaa gatcagctct agccatagga acatttggtg ggatgatgat 104820
 gacatttagg ccatagattt gactaaactc tactgcttca gtatctgctg ttctgtcat 104880
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 cattcttctt cggggcattg ttctacctgt atgctcatca atcaaaagaa cctcaccgtt 105060
 cctaaccaa taatccacat tctttttaaa taagaagctt gctctaagtg ttgcttgaac 105120
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 Nguyen, L.P., Jovanovich, S.B., Gates, C.M., Feldman, R.A., Spudich, J.L.,
 Spudich, E.N. and DeLong, E.F.
 <302> Bacterial rhodopsin: evidence for a new type of phototrophy in the
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 <303> Science
 <304> 289
 <305> 5486
 <306> 1902-1906
 <307> 2000-09-15
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<301> Beja,O., Aravind,L., Koonin,E.V., Suzuki,M.T., Hadd,A.,
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 Spudich,E.N. and DeLong,E.F.

<302> Bacterial rhodopsin: evidence for a new type of phototrophy in the
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<303> Science

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<306> 1902-1906

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24

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<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> light-driven proton pump; has the properties of a light-driven pr
 oton pump when expressed with retinal in Escherichia coli. Note
 that additional three nucleotide residues incorporated by pcr pri
 ming with reference to the original 31A08 DNA sequence (DNA resid
 ues 4-6, ggt), adding a new restriction site for cloning

<300>

<301> Beja,O., Aravind,L., Koonin,E.V., Suzuki,M.T.,
 Hadd,A.,Nguyen,L.P., Jovanovich,S.B., Gates,C.M.,
 Feldman,R.A.,Spudich,J.L., Spudich,E.N. and DeLong,E.F

<302> Bacterial rhodopsin: evidence for a new type of phototrophy in the
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<303> Science

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<309> 2000-06-15

<313> (1)..(750)

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1

5

10

15

48

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val 20 25 30	96
tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe 35 40 45	144
ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60	192
gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met 65 70 75 80	240
aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 85 90 95	288
att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu 100 105 110	336
att ctt gct gct gca act aat gtt gct gga tca tta ttt aag aaa tta Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu 115 120 125	384
cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 140	432
gga atc atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp 145 150 155 160	480
gta tac atg att tat gaa tta tgg gct gga gaa gga aaa tct gca tgt Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys 165 170 175	528
aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr 180 185 190	576
att atc atc ttt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly 195 200 205	624
tac ctg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr 210 215 220	672

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
 Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

aat gtt gct gtt aaa gaa tct tct aat gct 750
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 5
 <211> 250
 <212> PRT
 <213> Naturally occurring gamma proteobacterium

<400> 5

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 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 6
 <211> 747
 <212> DNA
 <213> Naturally occurring gamma proteobacterium

<220>
 <221> CDS
 <222> (1)..(747)
 <223> Native proteorhodopsin DNA sequence from BAC clone 31A08

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 <301> Beja, O., Aravind, L., Koonin, E.V., Suzuki, M.T., Hadd, A.,
 Nguyen, L.P., Jovanovich, S.B., Gates, C.M., Feldman, R.A., Spudich, J.L.,
 Spudich, E.N. and DeLong, E.F.
 <302> Bacterial rhodopsin: evidence for a new type of phototrophy in the
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 <303> Science
 <304> 289
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 <306> 1902-1906
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Met Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr Phe	
1 5 10 15	
gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt tct	96
Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val Ser	
20 25 30	
ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc ttt	144
Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe Phe	
35 40 45	
gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act gta	192
Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr Val	
50 55 60	
tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg aga	240
Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met Arg	
65 70 75 80	
ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac att	288
Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr Ile	
85 90 95	
gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta att	336
Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu Ile	
100 105 110	
ctt gct gct gca act aat gtt gct gga tca tta ttt aag aaa tta cta	384
Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu Leu	
115 120 125	
gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca gga	432
Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala Gly	
130 135 140	
atc atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg gta	480
Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp Val	
145 150 155 160	
tac atg att tat gaa tta tgg gct gga gaa gga aaa tct gca tgt aat	528
Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys Asn	
165 170 175	
act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat att	576
Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr Ile	
180 185 190	
atc .atc ttt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt tac	624

Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly Tyr
 195 200 205

ctg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat aac 672
 Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr Asn
 210 215 220

ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg aat 720
 Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp Asn
 225 230 235 240

gtt gct gtt aaa gaa tct tct aat gct 747
 Val Ala Val Lys Glu Ser Ser Asn Ala
 245

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 <213> Naturally occurring gamma proteobacterium
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Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val Ser
 20 25 30

Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe Phe
 35 40 45

Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr Val
 50 55 60

Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met Arg
 65 70 75 80

Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr Ile
 85 90 95

Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu Ile
 100 105 110

Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu Leu

115 120 125
 Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala Gly
 130 135 140
 Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp Val
 145 150 155 160
 Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys Asn
 165 170 175
 Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr Ile
 180 185 190
 Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly Tyr
 195 200 205
 Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr Asn
 210 215 220
 Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp Asn
 225 230 235 240
 Val Ala Val Lys Glu Ser Ser Asn Ala
 245

<210> 8
 <211> 750
 <212> DNA
 <213> Naturally occurring gamma proteobacterium

<220>
 <221> CDS
 <222> (1)..(750)
 <223> proteorhodopsin variant from clone EBAC40

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 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15
 ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96

Phe	Ala	Ala	Gly	Gly	Gly	Asp	Leu	Asp	Ala	Ser	Asp	Tyr	Thr	Gly	Val		
			20					25					30				
tct	ttt	tgg	tta	gtt	act	gct	gct	cta	tta	gca	tct	act	gta	ttt	ttc		144
Ser	Phe	Trp	Leu	Val	Thr	Ala	Ala	Leu	Leu	Ala	Ser	Thr	Val	Phe	Phe		
		35					40					45					
ttt	gtt	gaa	aga	gat	aga	gtt	tct	gca	aaa	tgg	aaa	aca	tca	tta	act		192
Phe	Val	Glu	Arg	Asp	Arg	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr		
	50					55					60						
gta	tcg	ggg	ctt	gtt	act	ggg	att	gct	ttc	tgg	cat	tac	atg	tac	atg		240
Val	Ser	Gly	Leu	Val	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Met	Tyr	Met		
65					70					75					80		
aga	ggg	gta	tgg	att	gag	act	ggg	gat	tcg	cca	act	gta	ttt	aga	tac		288
Arg	Gly	Val	Trp	Ile	Glu	Thr	Gly	Asp	Ser	Pro	Thr	Val	Phe	Arg	Tyr		
				85					90					95			
att	gat	tgg	tta	cta	aca	gtt	cct	cta	ttg	ata	tgt	gaa	ttc	tac	tta		336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu		
			100					105					110				
att	ctt	gct	gct	gca	aca	aat	gtt	gct	gct	ggc	ctg	ttt	aag	aaa	tta		384
Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Ala	Gly	Leu	Phe	Lys	Lys	Leu		
		115					120					125					
ttg	gtt	ggg	tct	ctt	gtt	atg	ctt	gtg	ttt	ggg	tac	atg	ggg	gag	gca		432
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala		
	130					135					140						
gga	att	atg	aac	gct	tgg	ggg	gca	ttc	gtt	att	ggg	tgt	tta	gct	tgg		480
Gly	Ile	Met	Asn	Ala	Trp	Gly	Ala	Phe	Val	Ile	Gly	Cys	Leu	Ala	Trp		
145					150					155					160		
gta	tac	atg	att	tat	gaa	cta	tgg	gct	gga	gaa	ggc	aag	gct	gca	tgt		528
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Trp	Ala	Gly	Glu	Gly	Lys	Ala	Ala	Cys		
				165					170					175			
aat	act	gca	agt	cct	gct	gtg	caa	tca	gct	tac	aac	aca	atg	atg	tat		576
Asn	Thr	Ala	Ser	Pro	Ala	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Tyr		
			180					185					190				
ata	atc	atc	ttt	ggg	tgg	gca	att	tat	cct	gta	ggg	tat	ttc	aca	ggg		624
Ile	Ile	Ile	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly		
		195					200					205					
tac	cta	atg	ggg	gac	ggg	gga	tca	gct	ctt	aac	tta	aac	ctt	atc	tat		672
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr		
	210					215					220						
gac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggg	tta	att	ata	tgg		720

Asp Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

aat gtt gct gtt aaa gaa tct tct aat gct
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

750

<210> 9
 <211> 250
 <212> PRT
 <213> Naturally occurring gamma proteobacterium

<400> 9

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Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp

145 150 155 160
 Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys
 165 170 175
 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190
 Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220
 Asp Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 10
 <211> 750
 <212> DNA
 <213> Naturally occurring gamma proteobacterium

 <220>
 <221> CDS
 <222> (1)..(750)
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 1 5 10 15

 ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

 tct ttt tgg tta gct act gct gct tta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Ala Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192

Phe	Val	Glu	Arg	Asp	Arg	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr		
50						55					60						
gta	tct	ggt	ctt	gtt	act	ggt	att	gct	ttc	tgg	cat	tac	atg	tac	atg	240	
Val	Ser	Gly	Leu	Val	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Met	Tyr	Met		
65					70					75					80		
aga	ggg	gta	tgg	att	gaa	act	ggt	gat	tcg	cca	act	gta	ttt	aga	tac	288	
Arg	Gly	Val	Trp	Ile	Glu	Thr	Gly	Asp	Ser	Pro	Thr	Val	Phe	Arg	Tyr		
				85					90					95			
att	gat	tgg	tta	cta	aca	gtt	cct	cta	tta	ata	tgt	gaa	ttc	tac	tta	336	
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu		
			100					105					110				
att	ctt	gct	gct	gct	act	aat	gtt	gct	gga	tca	tta	ttt	aag	aaa	tta	384	
Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Gly	Ser	Leu	Phe	Lys	Lys	Leu		
		115					120					125					
cta	gtt	ggt	tct	ctt	gtt	atg	ctt	gtg	ttt	ggt	tac	atg	ggt	gaa	gca	432	
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala		
	130					135					140						
gga	atc	atg	gct	gca	tgg	cct	gca	ttc	att	att	ggg	tgt	tta	gct	tgg	480	
Gly	Ile	Met	Ala	Ala	Trp	Pro	Ala	Phe	Ile	Ile	Gly	Cys	Leu	Ala	Trp		
145					150					155					160		
gta	tac	atg	att	tat	gaa	cta	tgg	gct	gga	gaa	gga	aaa	tct	gca	tgt	528	
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Trp	Ala	Gly	Glu	Gly	Lys	Ser	Ala	Cys		
				165					170					175			
aat	act	gca	agt	cct	gct	gtg	caa	tca	gct	tac	aac	aca	atg	atg	tat	576	
Asn	Thr	Ala	Ser	Pro	Ala	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Tyr		
			180					185					190				
att	atc	atc	ttt	ggt	tgg	gcg	att	tat	cct	gta	ggt	tat	ttc	aca	ggt	624	
Ile	Ile	Ile	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly		
			195				200					205					
tac	ctg	atg	ggt	gac	ggt	gga	tca	gct	ctt	aac	tta	aac	ctt	atc	tat	672	
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr		
	210					215					220						
aac	ctt	gct	gat	ttt	gtt	aac	aag	att	cta	ttt	ggt	tta	att	ata	tgg	720	
Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp		
225					230					235					240		
aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct							750	
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala								
				245					250								

<210> 11
 <211> 250
 <212> PRT
 <213> Naturally occurring gamma proteobacterium

<400> 11

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Ala Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr

180

185

190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 12
 <211> 750
 <212> DNA
 <213> Naturally occurring gamma proteobacterium

<220>
 <221> CDS
 <222> (1)..(750)
 <223> Proteorhodopsin variant from clone EBAC64

<400> 12
 atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15
 ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30
 tct ttt tgg tta gtt aca gct gct cta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45
 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80
 aga gga gta tgg att gaa act ggt gat tcg cct act gta ttt aga tac 288

Arg	Gly	Val	Trp	Ile	Glu	Thr	Gly	Asp	Ser	Pro	Thr	Val	Phe	Arg	Tyr		
				85					90					95			
att	gat	tgg	tta	cta	aca	gtt	cct	tta	tta	ata	tgt	gaa	ttc	tac	tta		336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu		
			100					105					110				
att	ctt	gct	gct	gca	act	aat	gtt	gcc	ggc	tca	tta	ttt	aag	aaa	ctt		384
Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Gly	Ser	Leu	Phe	Lys	Lys	Leu		
		115					120					125					
cta	gtt	ggg	tct	ctt	gtt	atg	ctt	gtg	ttt	ggg	tac	atg	ggg	gaa	gca		432
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala		
		130				135					140						
gga	att	atg	gca	gct	tgg	cct	gca	ttc	att	att	ggg	tgt	tta	gct	tgg		480
Gly	Ile	Met	Ala	Ala	Trp	Pro	Ala	Phe	Ile	Ile	Gly	Cys	Leu	Ala	Trp		
145					150				155					160			
gta	tac	atg	att	tat	gaa	cta	tat	gct	gga	gaa	gga	aaa	tct	gca	tgt		528
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Ala	Gly	Glu	Gly	Lys	Ser	Ala	Cys		
				165					170					175			
aat	act	gca	agt	cct	tcg	gtt	caa	tca	gct	tac	aac	aca	atg	atg	gct		576
Asn	Thr	Ala	Ser	Pro	Ser	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Ala		
			180					185					190				
atc	ata	gtc	ttc	ggg	tgg	gca	att	tat	cct	ata	ggg	tat	ttc	aca	ggg		624
Ile	Ile	Val	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Ile	Gly	Tyr	Phe	Thr	Gly		
		195				200						205					
tac	cta	atg	ggg	gac	ggg	gga	tca	gct	ctt	aac	tta	aac	ctt	att	tat		672
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr		
		210				215					220						
aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggg	tta	att	ata	tgg		720
Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp		
225					230					235				240			
aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct								750
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala								
				245				250									

<210> 13

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 13

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr

1	5	10	15
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val	20	25	30
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe	35	40	45
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	50	55	60
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met	65	70	75
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr	85	90	95
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu	100	105	110
Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu	115	120	125
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	130	135	140
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp	145	150	155
Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys	165	170	175
Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala	180	185	190
Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Ile Gly Tyr Phe Thr Gly	195	200	205
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr			

210

215

220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 14

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone HOT01m: GenBank# AF349978

<400> 14

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

tct ttt tgg tta gtt act gct gct cta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

gta tcg ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

aga ggg gta tgg att gag acc ggt gat tcg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

att gat tgg tta cta aca gtt cct cta ttg ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

att ctt gct gct gca aca aat gtt gct gct ggc ctg ttt aag aaa tta 384
 Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
 115 120 125

ttg gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gag gca 432
 Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

gga att atg aac gct tgg ggt gca ttc gtt att ggg tgt tta gct tgg 480
 Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp
 145 150 155 160

gta tac atg att tat gaa cta tgg gct gga gaa ggc aag gct gca tgt 528
 Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys
 165 170 175

aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat 576
 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

ata atc atc ttt ggt tgg gca att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
 Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

aat gtt gct gtt aaa gaa tct tct aat gct 750
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 15

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 15

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 16
<211> 753
<212> DNA
<213> Naturally occurring gamma prtoeobacterium

<220>
<221> CDS
<222> (1)..(753)
<223> Proteorhodopsin variant from pcr clone HOT75m1: GenBank#AF349979

<400> 16
atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20 25 30

tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt 144
Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt gct 192
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Ala
50 55 60

gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg 240
Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat 288
Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt 384
Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg 480
 Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160
 tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta 528
 Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175
 agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
 180 185 190
 att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205
 tac cta atg ggt ggc gaa ggt gta tac gct tca aac tta aac ctt ata 672
 Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220
 tat aac ctt gcc gac ctt gtt aac aag att cta ttt ggt ttg atc att 720
 Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240
 tgg aat gtt gct gtt aaa gaa tct tct aat gct 753
 Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 17
 <211> 251
 <212> PRT
 <213> Naturally occurring gamma prtoeobacterium
 <400> 17

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Ala
50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 18
<211> 753
<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone HOT75m3; GenBank#AF349980

<400> 18

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser	
1 5 10 15	
ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt	96
Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val	
20 25 30	
tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gta ttc ttt	144
Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe	
35 40 45	
ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act	192
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	
gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tac atg	240
Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met	
65 70 75 80	
aga ggt gtt tgg ata gat act ggt gat aca cca aca gta ttt aga tat	288
Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt	384
Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct	432
Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala	
130 135 140	
ggt tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg	480
Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp	
145 150 155 160	
tta tac atg att tat gag cta cat atg ggt gaa ggt aag gct gct gta	528
Leu Tyr Met Ile Tyr Glu Leu His Met Gly Glu Gly Lys Ala Ala Val	

165										170					175					
agt	act	gca	agt	cct	gct	gtt	aac	tct	gca	tac	aac	gca	atg	atg	aag	576				
Ser	Thr	Ala	Ser	Pro	Ala	Val	Asn	Ser	Ala	Tyr	Asn	Ala	Met	Met	Lys					
			180					185				190								
att	att	gtt	att	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggt	624				
Ile	Ile	Val	Ile	Gly	Trp	Ala	Ile	Tyr	Pro	Ala	Gly	Tyr	Ala	Ala	Gly					
		195					200					205								
tac	cta	atg	agt	ggt	gac	ggt	gta	tac	gct	tca	aac	tta	aac	ctt	ata	672				
Tyr	Leu	Met	Ser	Gly	Asp	Gly	Val	Tyr	Ala	Ser	Asn	Leu	Asn	Leu	Ile					
		210				215					220									
tat	aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggt	ttg	atc	att	720				
Tyr	Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile					
225					230				235					240						
tgg	aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct						753				
Trp	Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala										
				245					250											

<210> 19

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 19

Met	Gly	Lys	Leu	Leu	Leu	Ile	Leu	Gly	Ser	Ala	Ile	Ala	Leu	Pro	Ser
1				5					10					15	

Phe	Ala	Ala	Ala	Gly	Gly	Asp	Leu	Asp	Ile	Ser	Asp	Thr	Val	Gly	Val
			20					25					30		

Ser	Phe	Trp	Leu	Val	Thr	Ala	Gly	Met	Leu	Ala	Ala	Thr	Val	Phe	Phe
		35					40					45			

Phe	Val	Glu	Arg	Asp	Gln	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr
	50					55					60				

Val	Ser	Gly	Leu	Ile	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Leu	Tyr	Met
65					70					75				80	

Arg	Gly	Val	Trp	Ile	Asp	Thr	Gly	Asp	Thr	Pro	Thr	Val	Phe	Arg	Tyr
				85					90					95	

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu His Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Lys
180 185 190

Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 20

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone HOT75m4; GenBank #AF349981

<400> 20
 atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80

aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95

att gat tgg tta tta act gtt cca tta caa gtg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Val Val Glu Phe Tyr Leu
 100 105 110

att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125

cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140

gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg 480
 Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta 528
 Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175

agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
 180 185 190

att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly

195	200	205	
tac cta atg ggt ggc gaa ggt gta tac gct tca aac tta aac ctt ata			672
Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile			
210	215	220	
tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att			720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile			
225	230	235	240
tgg aat gtt gct gtt aaa gaa tct tct aat gct			753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala			
245	250		

<210> 21
 <211> 251
 <212> PRT
 <213> Naturally occurring gamma proteobacterium
 <400> 21

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Val Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 22

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone HOT75m8: GenBank#AF349982

<400> 22

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96

Phe	Ala	Ala	Ala	Gly	Gly	Asp	Leu	Asp	Ile	Ser	Asp	Thr	Val	Gly	Val		
			20					25					30				
tca	ttc	tgg	ctg	gtt	aca	gct	ggg	atg	tta	gcg	gca	act	gtg	ttc	ttt		144
Ser	Phe	Trp	Leu	Val	Thr	Ala	Gly	Met	Leu	Ala	Ala	Thr	Val	Phe	Phe		
		35					40					45					
ttt	gta	gaa	aga	gac	caa	gtc	agc	gct	aag	tgg	aaa	act	tca	ctt	act		192
Phe	Val	Glu	Arg	Asp	Gln	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr		
	50					55					60						
gta	tct	ggg	tta	att	act	ggg	ata	gct	ttt	tgg	cat	tat	ctc	tat	atg		240
Val	Ser	Gly	Leu	Ile	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Leu	Tyr	Met		
65					70					75					80		
aga	ggg	gtt	tgg	ata	gac	act	ggg	gat	acc	cca	aca	gta	ttc	aga	tat		288
Arg	Gly	Val	Trp	Ile	Asp	Thr	Gly	Asp	Thr	Pro	Thr	Val	Phe	Arg	Tyr		
				85					90					95			
att	gat	tgg	tta	tta	act	gtt	cca	tta	caa	atg	gtt	gag	ttc	tat	cta		336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Gln	Met	Val	Glu	Phe	Tyr	Leu		
			100					105					110				
att	ctt	gct	gct	tgt	aca	aat	gtt	gct	gct	tca	tta	ttt	aag	aag	ctt		384
Ile	Leu	Ala	Ala	Cys	Thr	Asn	Val	Ala	Ala	Ser	Leu	Phe	Lys	Lys	Leu		
		115					120					125					
cta	gct	ggg	tca	tta	gta	atg	tta	ggg	gct	gga	ttt	gca	ggc	gaa	gct		432
Leu	Ala	Gly	Ser	Leu	Val	Met	Leu	Gly	Ala	Gly	Phe	Ala	Gly	Glu	Ala		
	130					135					140						
gga	ttg	gct	cct	gta	tgg	cct	gct	ttc	att	att	ggg	atg	gct	gga	tgg		480
Gly	Leu	Ala	Pro	Val	Trp	Pro	Ala	Phe	Ile	Ile	Gly	Met	Ala	Gly	Trp		
145					150					155					160		
tta	tac	atg	att	tat	gag	cta	tat	atg	ggg	gaa	ggg	aag	gct	gct	gta		528
Leu	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Met	Gly	Glu	Gly	Lys	Ala	Ala	Val		
				165					170					175			
agt	act	gca	agt	cct	gct	gtt	aac	tct	gca	tac	aac	gca	atg	atg	gtg		576
Ser	Thr	Ala	Ser	Pro	Ala	Val	Asn	Ser	Ala	Tyr	Asn	Ala	Met	Met	Val		
			180					185					190				
att	att	gtt	gtt	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggg		624
Ile	Ile	Val	Val	Gly	Trp	Ala	Ile	Tyr	Pro	Ala	Gly	Tyr	Ala	Ala	Gly		
		195				200						205					
tac	cta	atg	ggg	ggc	gaa	ggg	gta	tac	gct	tca	aac	tta	aac	ctt	ata		672
Tyr	Leu	Met	Gly	Gly	Glu	Gly	Val	Tyr	Ala	Ser	Asn	Leu	Asn	Leu	Ile		
	210					215					220						
tat	aac	ctt	gcc	gac	ctt	gtt	aac	aag	att	cta	ttt	ggg	ttg	atc	att		720

Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

tgg aat gtt gct gtt aaa gaa tct tct aat gct
 Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

753

<210> 23
 <211> 251
 <212> PRT
 <213> Naturally occurring gamma proteobacterium

<400> 23

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140

Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp

145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Val
180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 24

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB0m1: GenBank#AF349983

<400> 24

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

tct ttt tgg tta gtt act gct gct cta tta gca tct act gta ttt ttc 144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192

Phe	Val	Glu	Arg	Asp	Arg	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr		
50						55					60						
gta	tct	ggt	ctt	gtt	act	ggt	att	gct	ttc	tgg	cat	tac	atg	tac	atg	240	
Val	Ser	Gly	Leu	Val	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Met	Tyr	Met		
65					70					75					80		
aga	ggg	gta	tgg	att	gag	act	ggt	gat	tcg	cca	act	gta	ttt	aga	tac	288	
Arg	Gly	Val	Trp	Ile	Glu	Thr	Gly	Asp	Ser	Pro	Thr	Val	Phe	Arg	Tyr		
				85					90					95			
att	gat	tgg	tta	cta	aca	gtt	cct	cta	ttg	ata	tgt	gaa	ttc	tac	tta	336	
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu		
			100					105					110				
att	ctt	gct	gct	gca	aca	aat	gtt	gct	gct	ggc	ctg	ttt	aag	aaa	tta	384	
Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Ala	Gly	Leu	Phe	Lys	Lys	Leu		
		115					120					125					
ttg	gtt	ggt	tct	ctt	gtt	atg	ctt	gtg	ttt	ggt	tac	atg	ggt	gag	gca	432	
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala		
	130					135					140						
gga	att	atg	aac	gct	tgg	cct	gca	ttc	att	att	ggg	tgt	tta	gct	tgg	480	
Gly	Ile	Met	Asn	Ala	Trp	Pro	Ala	Phe	Ile	Ile	Gly	Cys	Leu	Ala	Trp		
145					150					155					160		
gta	tac	atg	att	tat	gaa	cta	tat	gct	gga	gaa	gga	aaa	tct	gca	tgt	528	
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Ala	Gly	Glu	Gly	Lys	Ser	Ala	Cys		
				165					170					175			
aat	act	gca	agt	cct	tcg	gtt	caa	tca	gct	tac	aac	aca	atg	atg	gct	576	
Asn	Thr	Ala	Ser	Pro	Ser	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Ala		
			180					185					190				
atc	ata	gtc	ttc	ggt	tgg	gca	att	tat	cct	gta	ggt	tat	ttc	aca	ggt	624	
Ile	Ile	Val	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly		
		195					200					205					
tac	cta	atg	ggt	gac	ggt	gga	tca	gct	ctt	aac	tta	aac	ctt	att	tat	672	
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr		
	210					215					220						
aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggt	tta	att	ata	tgg	720	
Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp		
225					230					235					240		
aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct							750	
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala								
				245					250								

<210> 25
 <211> 250
 <212> PRT
 <213> Naturally occurring gamma proteobacterium

<400> 25

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

Gly Ile Met Asn Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175

Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala

180

185

190

Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 26
 <211> 750
 <212> DNA
 <213> Naturally occurring gamma proteobacterium

<220>
 <221> CDS
 <222> (1)..(750)
 <223> Proteorhodopsin variant from pcr clone MB0m2

<400> 26
 atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15
 ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30
 tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45
 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80
 aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac 288

Arg	Gly	Val	Trp	Ile	Glu	Thr	Gly	Asp	Ser	Pro	Thr	Val	Phe	Arg	Tyr		
				85					90					95			
att	gat	tgg	tta	cta	aca	gtt	cct	cta	tta	ata	tgt	gaa	ttc	tac	tta		336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu		
			100					105					110				
att	ctt	gct	gct	gct	act	aat	gtt	gct	gct	ggc	ctg	ttt	aag	aaa	tta		384
Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Ala	Gly	Leu	Phe	Lys	Lys	Leu		
		115					120					125					
ttg	gtt	ggg	tct	ctt	gtt	atg	ctt	gtg	ttt	ggg	tac	atg	ggg	gaa	gca		432
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala		
		130				135					140						
gga	att	atg	aac	gct	tgg	ggg	gca	ttc	gtt	att	ggg	tgt	tta	gct	tgg		480
Gly	Ile	Met	Asn	Ala	Trp	Gly	Ala	Phe	Val	Ile	Gly	Cys	Leu	Ala	Trp		
145					150					155					160		
gta	tac	atg	att	tat	gag	ctt	tgg	ctt	gga	gaa	gga	aaa	gct	gcg	tgt		528
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Trp	Leu	Gly	Glu	Gly	Lys	Ala	Ala	Cys		
				165					170					175			
aat	aca	gca	agt	cct	gct	gtt	cag	tca	gct	tac	aac	aca	atg	atg	atg		576
Asn	Thr	Ala	Ser	Pro	Ala	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Met		
			180					185					190				
atc	atc	atc	ttt	ggg	tgg	gca	att	tat	cct	gta	ggg	tat	ttc	aca	ggg		624
Ile	Ile	Ile	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly		
		195					200					205					
tac	cta	atg	ggg	gac	ggg	gga	tca	gca	ctt	aac	tta	aac	ctt	atc	tat		672
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr		
		210				215					220						
aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggg	tta	att	ata	tgg		720
Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp		
225					230					235					240		
aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct								750
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala								
				245					250								

<210> 27

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 27

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr

1	5	10	15												
Phe	Ala	Ala	Gly	Gly	Gly	Asp	Leu	Asp	Ala	Ser	Asp	Tyr	Thr	Gly	Val
			20					25						30	
Ser	Phe	Trp	Leu	Val	Thr	Ala	Ala	Leu	Leu	Ala	Ser	Thr	Val	Phe	Phe
		35					40					45			
Phe	Val	Glu	Arg	Asp	Arg	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr
	50					55					60				
Val	Ser	Gly	Leu	Val	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Met	Tyr	Met
65					70					75					80
Arg	Gly	Val	Trp	Ile	Glu	Thr	Gly	Asp	Ser	Pro	Thr	Val	Phe	Arg	Tyr
				85					90					95	
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu
			100					105						110	
Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Ala	Gly	Leu	Phe	Lys	Lys	Leu
		115					120						125		
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala
	130					135					140				
Gly	Ile	Met	Asn	Ala	Trp	Gly	Ala	Phe	Val	Ile	Gly	Cys	Leu	Ala	Trp
145					150					155					160
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Trp	Leu	Gly	Glu	Gly	Lys	Ala	Ala	Cys
				165					170					175	
Asn	Thr	Ala	Ser	Pro	Ala	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Met
			180					185					190		
Ile	Ile	Ile	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly
		195					200					205			
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr

210

215

220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 28

<211> 750

<212> DNA

<213> Naturally occuring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB20m2; GenBank #AF349985

<400> 28

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

att ctt gct gct gca act aat gtt gct gct ggc ctg ttt aag aaa tta 384
 Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
 115 120 125

ttg gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gag gca 432
 Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

gga att atg aac gct tgg ggt gca ttc gtt att ggg tgt tta gct tgg 480
 Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp
 145 150 155 160

gta tac atg att tat gaa cta tgg gct gga gaa ggc aag gct gca tgt 528
 Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys
 165 170 175

aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat 576
 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

ata atc atc ttt ggt tgg gca att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
 Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

aat gtt gct gtt aaa gaa tct tct aat gct 750
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 29

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 29

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 30
<211> 750
<212> DNA
<213> Naturally occurring gamma proteobacterium

<220>
<221> CDS
<222> (1)..(750)
<223> Proteorhodopsin variant from pcr clone MB20m5; GenBank#AF349986

<400> 30
atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt 96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

tct ttt tgg tta gtt aca gct gct cta tta gca tct act gta ttt ttc 144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac 288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta 336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

att ctt gct gct gct act aat gtt gct gga tca tta ttt aag aaa tta 384
Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120 125

cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca 432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

caa att atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg 480
 Gln Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
 145 150 155 160
 gta tac atg att tat gaa cta tat gct gga gaa gga aaa tct gca tgt 528
 Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175
 aat act gca agt cct tcg gtt caa tca gct tac aac aca atg atg gct 576
 Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala
 180 185 190
 atc ata gtc ttc ggt tgg gca att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205
 tac cta atg ggt gac ggt ggg tca gct ctt aac tta aac ctt att tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220
 aac ctt gct gac ttt gtt aac aag att cta ctt ggt tta att ata tgg 720
 Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Leu Gly Leu Ile Ile Trp
 225 230 235 240
 aat gtt gct gtt aaa gaa tct tct aat gct 750
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 31

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 31

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gln Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala
180 185 190

Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Leu Gly Leu Ile Ile Trp
225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 32

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB20m12; GenBank #AF349987

<400> 32

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr	
1 5 10 15	
ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt	96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val	
20 25 30	
tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc	144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe	
35 40 45	
ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act	192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	
gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg	240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met	
65 70 75 80	
aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac	288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct gca gct aat gtt gct gga tca tta ttt aag aaa tta	384
Ile Leu Ala Ala Ala Ala Asn Val Ala Gly Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	
gga atc atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg	480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp	
145 150 155 160	
gta tac atg att tat gaa tta tgg gct gga gaa gga aaa tct gca tgt	528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys	
165 170 175	

aat act gca agt cct gct gtg caa tca gcc tac aac aca atg atg tat 576
 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

att atc atc ttt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

tac ttg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
 Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

aat gtt gct gtt aaa gaa tct tct aat gct 750
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 33

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 33

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Ala Ala Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 34

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB40m1; GenBank #AF349988

<400> 34
 atg ggt aaa tta tta ctg ata ata ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Leu Ile Ile Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

tct ttt tgg tta gtt aca gct gct cta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

aga gga gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

att ctt gct gct gca act aat gtt gcc ggc tca tta ttt aag aaa ctt 384
 Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
 115 120 125

cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca 432
 Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

gga att atg gca gct tgg cct gca ttc att att ggg tgt tta gct tgg 480
 Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
 145 150 155 160

gta tat atg att tat gaa cta tat gct gga gaa gga aaa tct gca tgt 528
 Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175

aat aca gca agt cct gct gtg caa tca gct tac aac aca atg atg tat 576
 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

att atc gtc ttt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

tac ctg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
 Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

aat gtt gct gtt aaa gaa tct tct aat gct 750
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 35

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 35

Met Gly Lys Leu Leu Leu Ile Ile Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 36

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB40m5;p GenBank #AF349989

<400> 36

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

tct ttt tgg tta gtt act gct gct cta tta gca tct act gta ttt ttc	144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe	
35 40 45	
ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act	192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	
gta tcg ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg	240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met	
65 70 75 80	
aga ggg gta tgg att gag act ggt gat tcg cca act gta ttt aga tac	288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta cta aca gtt cct cta ttg ata tgt gaa ttc tac tta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct gca aca aat gtt gct gct ggc ctg ttt aag aaa tta	384
Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu	
115 120 125	
ttg gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gag gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	
gga att atg aac gct tgg ggt gca ttc gtt att ggg tgt tta gct tgg	480
Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp	
145 150 155 160	
gta tac atg att tat gaa cta tgg gct gga gaa ggc aag gct gca tgt	528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys	
165 170 175	
aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat	576
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr	
180 185 190	
ata atc atc ttt ggt tgg gca att tat cct gta ggt tat ttc aca ggt	624
Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly	
195 200 205	
tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat	672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr	
210 215 220	
aac ctt gct gac ttt gtt aac aag aat cta ttt ggt tta att ata tgg	720
Asn Leu Ala Asp Phe Val Asn Lys Asn Leu Phe Gly Leu Ile Ile Trp	
225 230 235 240	

aat gtt gct gtt aaa gaa tct tct aat gct
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

750

<210> 37
 <211> 250
 <212> PRT
 <213> Naturally occurring gamma proteobacterium
 <400> 37

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp
 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys
 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Asn Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 38

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB40m12; GenBank # AF34999

<400> 38

atg ggt aaa tta tta cgg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Arg Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

tct ttt tgg tta gtt aca gct gct cta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr

50	55	60	
gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tat atg			240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met			
65	70	75	80
aga gga gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac			288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr			
	85	90	95
att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta			336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu			
	100	105	110
att ctt gct gct gca act aat gtt gct gga tca tta ttt aag aaa tta			384
Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu			
	115	120	125
cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca			432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala			
	130	135	140
gga atc atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg			480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp			
145	150	155	160
gta tac atg att tat gaa cta tgg gct gga gaa gga aaa tct gca tgt			528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys			
	165	170	175
aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat			576
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr			
	180	185	190
atc atc atc gtt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt			624
Ile Ile Ile Val Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly			
	195	200	205
tac ctg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat			672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr			
	210	215	220
aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg			720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp			
225	230	235	240
aat gtt gct gtt aaa gaa tct tct aat gct			750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala			
	245	250	

<210> 39

<211> 250
<212> PRT
<213> Naturally occurring gamma proteobacterium

<400> 39

Met Gly Lys Leu Leu Arg Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
180 185 190

Ile Ile Ile Val Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 40

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB100m5; GenBank #AF349991

<400> 40

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt 96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

tct ttt tgg tta gtt aca gct gct cta tta gca tct act gta ttt ttc 144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

aga gga gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac 288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr

	85	90	95	
att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta				336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu				
	100	105	110	
att ctt gct gct gca act aat gtt gcc ggc tca tta ttt aag aaa ctt				384
Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu				
	115	120	125	
cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca				432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala				
	130	135	140	
gga att atg gca gct tgg cct gca ttc att att ggg tgt tta gct tgg				480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp				
	145	150	155	160
gta tac atg att tat gaa cta tat gct gga gaa gga aaa tct gca tgt				528
Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys				
	165	170	175	
aat act gca agt cct tcg gtt caa tca gct tac aac aca atg atg gct				576
Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala				
	180	185	190	
atc ata gtc ttc ggt tgg gca att tat cct gta ggt tat ttc aca ggt				624
Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly				
	195	200	205	
tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt att tat				672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr				
	210	215	220	
aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg				720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp				
	225	230	235	240
aat gtt gct gtt aaa gaa tct tct aat gct				750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala				
	245	250		

<210> 41

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 41

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala
180 185 190

Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 42

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB100m7; GenBank #AF349992

<400> 42

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

att ctt gct gct gct act aat gtt gcc ggc tca tta ttt aag aaa ctt 384
 Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu

115	120	125	
cta gtt ggt tct ctt gtt atg	ctt gtg ttt ggt	tac atg ggt gaa gca	432
Leu Val Gly Ser Leu Val Met	Leu Val Phe Gly Tyr Met Gly Glu Ala		
130	135	140	
gga att atg gca gct tgg cct gca ttc att att	ggg tgt tta gct tgg		480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile	Gly Cys Leu Ala Trp		
145	150	155	160
gta tac atg att tat gaa cta tat gct gga gaa gga aaa tct gca tgt			528
Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys			
165	170	175	
aat act gca agt cct tcg gtt caa tca gct tac aac aca atg atg gct			576
Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala			
180	185	190	
atc ata gtc ttc ggt tgg gca att tat cct gta ggt tat ttc aca ggt			624
Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly			
195	200	205	
tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt att tat			672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr			
210	215	220	
aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg			720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp			
225	230	235	240
aat gct gct gtt aaa gaa tct tct aat gct			750
Asn Ala Ala Val Lys Glu Ser Ser Asn Ala			
245	250		

<210> 43

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 43

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala
180 185 190

Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
225 230 235 240

Asn Ala Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 44
 <211> 750
 <212> DNA
 <213> Naturally occurring gamma proteobacterium

 <220>
 <221> CDS
 <222> (1)..(750)
 <223> Proteorhodopsin variant from pcr clone MB100m9; GenBank #AF349993

 <400> 44
 atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

 ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

 tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

 ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
 Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

 gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tat atg 240
 Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

 aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac 288
 Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

 ata gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

 att ctt gcc gct gca act aat gtt gct gga tca tta ttt aag aaa tta 384
 Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
 115 120 125

 ctt gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca 432
 Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

 gga atc atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg 480
 Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp

145	150	155	160	
gta tac atg att tat gaa cta tgg gct gga gaa gga aaa tct gca tgt				528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys	165	170	175	
aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat				576
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr	180	185	190	
atc atc atc ttt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt				624
Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly	195	200	205	
tac ctt atg ggt gac ggt gga tca gca ctt aac tta aac ctt att tat				672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr	210	215	220	
aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg				720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp	225	230	235	240
aat gtt gct gtt aaa gaa tct tct aat gct				750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala	245	250		

<210> 45
 <211> 250
 <212> PRT
 <213> Naturally occurring gamma proteobacterium

<400> 45

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 46

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB100m10; GenBank #AF34999

<400> 46

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr	
1 5 10 15	

ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt	96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val	
20 25 30	

tct ttt tgg tta gtt aca gct gct cta tta gcg tct act gta ttt ttc	144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe	
35 40 45	

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act	192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tat atg	240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met	
65 70 75 80	

aga gga gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac	288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr	
85 90 95	

att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu	
100 105 110	

att ctt gct gct gca act aat gtt gcc ggc tca tta ttt aag aaa ctt	384
Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu	
115 120 125	

cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	

gga ata atg gcg gct tgg cct gca ttc atc gtt gga tgt tta gca tgg	480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Val Gly Cys Leu Ala Trp	
145 150 155 160	

gta tat atg att tat gaa cta tgg gct ggt gaa gga aaa tct gca tgt	528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys	
165 170 175	

aat act gca agt cct gct gta cag tca gct tac aac aca atg atg tat	576
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Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190
 atc atc atc gtt ggt tgg gca att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Ile Val Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205
 tac cta atg ggt gac ggt gga tca gct ctt aat cta aac ctt att tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220
 aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
 Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240
 aat gtt gct gtt aaa gaa tct tct aat gct 750
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 47
 <211> 250
 <212> PRT
 <213> Naturally occurring gamma proteobacterium
 <400> 47

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu

100

105

110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Val Gly Cys Leu Ala Trp
 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

Ile Ile Ile Val Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 48

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PALB1; GenBank #AF349995

<400> 48

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca

48

Met	Gly	Lys	Leu	Leu	Leu	Ile	Leu	Gly	Ser	Ala	Ile	Ala	Leu	Pro	Ser		
1				5					10					15			
ttt	gct	gct	gct	ggt	ggc	gat	cta	gat	ata	agt	gat	act	ggt	ggt	ggt		96
Phe	Ala	Ala	Ala	Gly	Gly	Asp	Leu	Asp	Ile	Ser	Asp	Thr	Val	Gly	Val		
			20					25					30				
tca	ttc	tgg	ctg	ggt	aca	gct	ggt	atg	tta	gcg	gca	act	gta	ttc	ttt		144
Ser	Phe	Trp	Leu	Val	Thr	Ala	Gly	Met	Leu	Ala	Ala	Thr	Val	Phe	Phe		
		35					40					45					
ttt	gta	gaa	aga	gac	caa	gtc	agc	gct	aag	tgg	aaa	act	tca	ctt	act		192
Phe	Val	Glu	Arg	Asp	Gln	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr		
	50					55					60						
gta	tct	ggt	tta	att	act	ggt	ata	gct	ttt	tgg	cat	tat	ctc	tac	atg		240
Val	Ser	Gly	Leu	Ile	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Leu	Tyr	Met		
65					70				75						80		
aga	ggt	ggt	tgg	ata	gat	act	ggt	gat	aca	cca	aca	gta	ttt	aga	tat		288
Arg	Gly	Val	Trp	Ile	Asp	Thr	Gly	Asp	Thr	Pro	Thr	Val	Phe	Arg	Tyr		
				85				90						95			
att	gat	tgg	cta	tta	act	ggt	cca	tta	caa	atg	ggt	gag	ttc	tat	cta		336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Gln	Met	Val	Glu	Phe	Tyr	Leu		
			100					105					110				
att	ctt	gct	gct	tgt	aca	agt	ggt	gct	gct	tca	tta	ttt	aag	aag	ctt		384
Ile	Leu	Ala	Ala	Cys	Thr	Ser	Val	Ala	Ala	Ser	Leu	Phe	Lys	Lys	Leu		
		115					120					125					
cta	gct	ggt	tca	tta	gta	atg	tta	ggt	gct	gga	ttt	gca	ggc	gaa	gct		432
Leu	Ala	Gly	Ser	Leu	Val	Met	Leu	Gly	Ala	Gly	Phe	Ala	Gly	Glu	Ala		
		130				135					140						
ggt	tta	gct	cct	gta	tta	cct	gct	ttc	att	ctt	ggt	atg	gct	ggt	tgg		480
Gly	Leu	Ala	Pro	Val	Leu	Pro	Ala	Phe	Ile	Leu	Gly	Met	Ala	Gly	Trp		
145					150					155					160		
tta	tac	atg	att	tat	gag	cta	cat	atg	ggt	gaa	ggt	aag	gct	gct	gta		528
Leu	Tyr	Met	Ile	Tyr	Glu	Leu	His	Met	Gly	Glu	Gly	Lys	Ala	Ala	Val		
				165					170					175			
agt	act	gca	agt	cct	gct	ggt	aac	tct	gct	tac	aat	gca	atg	atg	aag		576
Ser	Thr	Ala	Ser	Pro	Ala	Val	Asn	Ser	Ala	Tyr	Asn	Ala	Met	Met	Lys		
			180					185					190				
att	att	ggt	att	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggt		624
Ile	Ile	Val	Ile	Gly	Trp	Ala	Ile	Tyr	Pro	Ala	Gly	Tyr	Ala	Ala	Gly		
		195				200						205					
tac	cta	atg	agt	ggt	gac	ggt	gta	tac	gct	tca	aac	tta	aac	ctt	ata		672

Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220
 tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att 720
 Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240
 tgg aat gtt gct gtt aaa gaa tct tct aat gct 753
 Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 49
 <211> 251
 <212> PRT
 <213> Naturally occurring gamma proteobacterium
 <400> 49

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala

130

135

140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Leu Gly Met Ala Gly Trp
 145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu His Met Gly Glu Gly Lys Ala Ala Val
 165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Lys
 180 185 190

Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 50

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PALB2; GenBank #AF349996

<400> 50

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt 144

Ser	Phe	Trp	Leu	Val	Thr	Ala	Gly	Met	Leu	Ala	Ala	Thr	Val	Phe	Phe	
		35					40					45				
ttt	gta	gaa	aga	gac	caa	gtc	agc	gct	gag	tgg	aaa	act	tca	ctt	act	192
Phe	Val	Glu	Arg	Asp	Gln	Val	Ser	Ala	Glu	Trp	Lys	Thr	Ser	Leu	Thr	
	50					55					60					
gta	tct	ggg	tta	att	act	ggg	ata	gct	ttt	tgg	cat	tat	ctc	tat	atg	240
Val	Ser	Gly	Leu	Ile	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Leu	Tyr	Met	
65					70					75					80	
aga	ggg	gtt	tgg	ata	gat	act	ggg	gat	acc	cca	aca	gta	ttc	aga	tat	288
Arg	Gly	Val	Trp	Ile	Asp	Thr	Gly	Asp	Thr	Pro	Thr	Val	Phe	Arg	Tyr	
				85					90					95		
att	gat	tgg	tta	tta	act	gtt	cca	tta	caa	atg	gtt	gag	ttc	tat	cta	336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Gln	Met	Val	Glu	Phe	Tyr	Leu	
			100					105					110			
att	ctt	gct	gct	tgt	aca	agt	gtt	gct	gct	tca	tta	ttt	aag	aag	ctt	384
Ile	Leu	Ala	Ala	Cys	Thr	Ser	Val	Ala	Ala	Ser	Leu	Phe	Lys	Lys	Leu	
		115					120					125				
cta	gct	ggg	tca	tta	gta	atg	tta	ggg	gct	gga	ttt	gca	ggc	gaa	gct	432
Leu	Ala	Gly	Ser	Leu	Val	Met	Leu	Gly	Ala	Gly	Phe	Ala	Gly	Glu	Ala	
	130					135					140					
gga	tta	gct	cct	gta	tta	cct	gct	ttc	att	att	ggg	atg	gct	gga	tgg	480
Gly	Leu	Ala	Pro	Val	Leu	Pro	Ala	Phe	Ile	Ile	Gly	Met	Ala	Gly	Trp	
145					150				155						160	
tta	tac	atg	att	tat	gag	cta	tat	atg	ggg	gaa	ggg	aag	gct	gct	gta	528
Leu	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Met	Gly	Glu	Gly	Lys	Ala	Ala	Val	
				165					170					175		
agt	act	gca	agt	cct	gct	gtt	aac	tct	gca	tac	aac	gca	atg	atg	atg	576
Ser	Thr	Ala	Ser	Pro	Ala	Val	Asn	Ser	Ala	Tyr	Asn	Ala	Met	Met	Met	
			180					185					190			
att	att	gtt	gtt	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggg	624
Ile	Ile	Val	Val	Gly	Trp	Ala	Ile	Tyr	Pro	Ala	Gly	Tyr	Ala	Ala	Gly	
		195					200					205				
tac	cta	atg	ggg	ggc	gaa	ggg	gta	tac	gct	tca	aac	tta	aac	ctt	ata	672
Tyr	Leu	Met	Gly	Gly	Glu	Gly	Val	Tyr	Ala	Ser	Asn	Leu	Asn	Leu	Ile	
	210					215					220					
tat	aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggg	ttg	atc	att	720
Tyr	Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	
225					230					235					240	
tgg	aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct						753

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 51
<211> 251
<212> PRT
<213> Naturally occurring gamma proteobacterium

<400> 51

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Glu Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val

165

170

175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
 180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 52

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PALB5; GenBank#AF349997

<400> 52

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

gta tct ggt tta att act ggt ata gcc ttt tgg cat tat ctc tat atg 240

Val	Ser	Gly	Leu	Ile	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Leu	Tyr	Met	
65					70				75						80	
aga	ggt	ggt	tgg	ata	gac	act	ggt	gat	acc	cca	aca	gta	ttc	aga	tat	288
Arg	Gly	Val	Trp	Ile	Asp	Thr	Gly	Asp	Thr	Pro	Thr	Val	Phe	Arg	Tyr	
				85					90					95		
att	gat	tgg	tta	tta	act	ggt	cca	tta	caa	atg	ggt	gag	ttc	tat	cta	336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Gln	Met	Val	Glu	Phe	Tyr	Leu	
			100					105					110			
att	ctt	gct	gct	tgt	aca	aat	ggt	gct	gct	tca	tta	ttt	aag	aag	ctt	384
Ile	Leu	Ala	Ala	Cys	Thr	Asn	Val	Ala	Ala	Ser	Leu	Phe	Lys	Lys	Leu	
		115					120					125				
cta	gct	ggt	tca	tta	gta	atg	tta	ggt	gct	gga	ttt	gca	ggc	gaa	gct	432
Leu	Ala	Gly	Ser	Leu	Val	Met	Leu	Gly	Ala	Gly	Phe	Ala	Gly	Glu	Ala	
	130					135				140						
gga	tta	gct	cct	gta	tgg	cct	gct	ttc	att	att	ggt	atg	gct	gga	tgg	480
Gly	Leu	Ala	Pro	Val	Trp	Pro	Ala	Phe	Ile	Ile	Gly	Met	Ala	Gly	Trp	
145					150				155					160		
tta	tac	atg	att	tat	gag	cta	tat	atg	ggt	gaa	ggt	aag	gct	gct	gta	528
Leu	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Met	Gly	Glu	Gly	Lys	Ala	Ala	Val	
				165					170					175		
agt	act	gca	agt	cct	gct	ggt	aac	tct	gca	tac	aac	gca	atg	atg	atg	576
Ser	Thr	Ala	Ser	Pro	Ala	Val	Asn	Ser	Ala	Tyr	Asn	Ala	Met	Met	Met	
			180					185					190			
att	att	ggt	ggt	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggt	624
Ile	Ile	Val	Val	Gly	Trp	Ala	Ile	Tyr	Pro	Ala	Gly	Tyr	Ala	Ala	Gly	
		195				200						205				
tac	cta	atg	ggt	ggc	gaa	ggt	gta	tac	gct	tca	aac	cta	aac	ctt	ata	672
Tyr	Leu	Met	Gly	Gly	Glu	Gly	Val	Tyr	Ala	Ser	Asn	Leu	Asn	Leu	Ile	
	210					215					220					
tat	aac	ctt	gct	gac	ttt	ggt	aac	aag	att	cta	ttt	ggt	ttg	atc	att	720
Tyr	Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	
225				230					235					240		
tgg	aat	ggt	gct	ggt	aaa	gaa	tct	tct	aat	gct						753
Trp	Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala						
				245					250							

<210> 53

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 53

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140

Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
 180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly

195	200	205
Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile		
210	215	220
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile		
225	230	235 240
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala		
245	250	

<210> 54
 <211> 753
 <212> DNA
 <213> Naturally occurring gamma proteobacterium

 <220>
 <221> CDS
 <222> (1)..(753)
 <223> Proteorhodopsin variant from pcr clone PalB7; GenBank #AF349999

<400> 54	
atg ggt aaa tta tta ctg ata tta ggt agt gct att gcg ctt cca tca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser	
1 5 10 15	
ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt	96
Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val	
20 25 30	
tca ttc tgg ctg gtt acg gct ggt atg tta gcg gca act gta ttc ttt	144
Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe	
35 40 45	
ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act	192
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	
gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tac atg	240
Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met	
65 70 75 80	
aga ggt gtt tgg ata gat act ggt gat aca cca aca gta ttt aga tat	288
Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta	336

Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Gln	Met	Val	Glu	Phe	Tyr	Leu		
			100					105					110				
att	ctt	gcc	gct	tgt	aca	agt	gtt	gct	gct	tca	tta	ttt	aag	aag	ctt		384
Ile	Leu	Ala	Ala	Cys	Thr	Ser	Val	Ala	Ala	Ser	Leu	Phe	Lys	Lys	Leu		
		115					120					125					
cta	gct	ggt	tca	ttg	gta	atg	tta	ggt	gct	gga	tct	gca	ggc	gaa	gct		432
Leu	Ala	Gly	Ser	Leu	Val	Met	Leu	Gly	Ala	Gly	Ser	Ala	Gly	Glu	Ala		
		130				135					140						
gga	tta	gct	cct	gta	tta	cct	gct	ttc	att	att	ggt	atg	gct	gga	tgg		480
Gly	Leu	Ala	Pro	Val	Leu	Pro	Ala	Phe	Ile	Ile	Gly	Met	Ala	Gly	Trp		
145					150				155						160		
tta	tac	atg	att	tat	gag	cta	tat	atg	ggt	gaa	ggt	aag	gct	gct	gta		528
Leu	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Met	Gly	Glu	Gly	Lys	Ala	Ala	Val		
				165					170						175		
agt	act	gca	agt	cct	gct	gtt	aac	tct	gca	tac	aac	gca	atg	atg	atg		576
Ser	Thr	Ala	Ser	Pro	Ala	Val	Asn	Ser	Ala	Tyr	Asn	Ala	Met	Met	Met		
			180					185					190				
att	att	gtt	gtt	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggt		624
Ile	Ile	Val	Val	Gly	Trp	Ala	Ile	Tyr	Pro	Ala	Gly	Tyr	Ala	Ala	Gly		
		195					200					205					
tac	cta	atg	ggt	ggc	gaa	ggt	gta	tac	gct	tca	aac	tta	aac	ctc	ata		672
Tyr	Leu	Met	Gly	Gly	Glu	Gly	Val	Tyr	Ala	Ser	Asn	Leu	Asn	Leu	Ile		
		210				215					220						
tat	aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggt	ttg	atc	att		720
Tyr	Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile		
225					230				235						240		
tgg	aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct							753
Trp	Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala							
				245					250								

<210> 55

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 55

Met	Gly	Lys	Leu	Leu	Leu	Ile	Leu	Gly	Ser	Ala	Ile	Ala	Leu	Pro	Ser
1				5				10					15		

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val

20	25	30
Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe		
35	40	45
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr		
50	55	60
Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met		
65	70	75
Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr		
85	90	95
Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu		
100	105	110
Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu		
115	120	125
Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Ser Ala Gly Glu Ala		
130	135	140
Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp		
145	150	155
Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val		
165	170	175
Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met		
180	185	190
Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly		
195	200	205
Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile		
210	215	220
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile		

225

230

235

240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 56

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PalB6; GenBank # AF349998

<400> 56

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80

aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95

att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

att ctt gct gct tgt aca aat gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125

cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140

gga tta gct cct gta tgg cct gct ttc att att ggt atg gct gga tgg 480
 Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta 528
 Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175

agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg gtg 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Val
 180 185 190

att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

tac cta atg ggt ggc gaa ggt gta tac gct tca aac cta aac ctt ata 672
 Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att 720
 Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

tgg aat gtt gct gtt aaa gaa tct tct aat gct 753
 Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 57

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 57

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Val
180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 58
 <211> 753
 <212> DNA
 <213> Naturally occurring gamma proteobacteria
 <220>
 <221> CDS
 <222> (1)..(753)
 <223> Proteorhodopsin variant from pcr clone PalB8; GenBank #AF350000

<400> 58
 atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15
 ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30
 tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45
 ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60
 gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80
 aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95
 att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110
 att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt 384
 Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125
 cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct 432
 Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140
 gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg 480
 Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta 528
 Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175

agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
 180 185 190

att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

tac cta atg ggt ggc gaa ggt gta tac gct tca aac tta aac ctt ata 672
 Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

tat aac ctt gct gac ctt gtt aac aag att cta ttt ggt ttg atc att 720
 Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

tgg aat gtt gct gtt aaa gaa tct tct aat gct 753
 Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 59

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacteria

<400> 59

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 60

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacteria

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PalE1;GenBank# AF350001

<400> 60

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser	
1 5 10 15	
ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt	96
Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val	
20 25 30	
tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt	144
Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe	
35 40 45	
ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act	192
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	
gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg	240
Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met	
65 70 75 80	
aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat	288
Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta tta act gtt cca tta caa gtg gtt gag ttc tat cta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Val Val Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt	384
Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct	432
Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala	
130 135 140	
gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg	480
Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp	
145 150 155 160	
tta tac atg att tat gag cta tat atg ggt gaa ggc aag gct gct gta	528
Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val	
165 170 175	
agt act gca agt cct gct gtt aac cct gca tac aac gca atg atg atg	576
Ser Thr Ala Ser Pro Ala Val Asn Pro Ala Tyr Asn Ala Met Met Met	
180 185 190	

att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

tac cta atg ggt ggc gaa ggt gta tac gct tca aac tta aac ctt ata 672
 Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att 720
 Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

tgg aat gtt gct gtt aaa gaa tct tct aat gct 753
 Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 61
 <211> 251
 <212> PRT
 <213> Naturally occurring gamma proteobacteria
 <400> 61

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Val Val Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Pro Ala Tyr Asn Ala Met Met Met
 180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 62

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PalE6; GenBank#AF350002

<400> 62

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

48

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt	96
Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val	
20 25 30	
tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gta ttc ttt	144
Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe	
35 40 45	
ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act	192
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	
gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tac atg	240
Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met	
65 70 75 80	
aga ggt gtt tgg ata gat act ggt gat aca cca aca gta ttt aga tat	288
Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt	384
Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct	432
Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala	
130 135 140	
ggt tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg	480
Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp	
145 150 155 160	
tta tac atg att tat gag cta cat atg ggt gaa ggt aag gct gct gta	528
Leu Tyr Met Ile Tyr Glu Leu His Met Gly Glu Gly Lys Ala Ala Val	
165 170 175	
agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg aag	576
Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Lys	
180 185 190	
att att gtt att gga tgg gca att tat cct gct gga tat gct gct ggt	624
Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly	
195 200 205	
tac cta atg agt ggt gac ggt gta tac gct tca aac tta aac ctt ata	672
Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile	
210 215 220	

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att 720
 Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

tgg aat gtt gct gtt aaa gaa tct tct aat gct 753
 Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 63

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 63

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu His Met Gly Glu Gly Lys Ala Ala Val
 165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Lys
 180 185 190

Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 64

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PalE7; GenBank# AF350003

<400> 64

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act	192
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	
gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg	240
Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met	
65 70 75 80	
aga ggt gtt tgg ata gat act ggt gat acc cca aca gta ttc aga tat	288
Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt	384
Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct	432
Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala	
130 135 140	
gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg	480
Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp	
145 150 155 160	
cta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta	528
Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val	
165 170 175	
agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg	576
Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met	
180 185 190	
att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt	624
Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly	
195 200 205	
tac cta atg ggt ggc gaa ggc gta tac gct tca aac tta aac ctt ata	672
Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile	
210 215 220	
tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att	720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile	
225 230 235 240	
tgg aat gtt gct gtt aaa gaa tct tct aat gct	753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala	
245 250	

<210> 65
 <211> 251
 <212> PRT
 <213> Naturally occurring gamma proteobacterium

<400> 65

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
 130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250